

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 07:52:30 ; Search time 1498 Seconds  
(without alignments)  
518.880 Million cell updates/sec

Title: US-09-606-804-1  
Perfect score: 19  
Sequence: 1 ccaatnnnnnnnnccacg 19

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl :

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- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
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- 9: gb.pr.\*
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- 34: em.htg\_pln.\*
- 35: em.htg\_rtd.\*
- 36: em.htg\_mam.\*
- 37: em.htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	10	52.6	19	6	AR274677 Sequence
2	10	52.6	19	6	AX275341 Sequence
3	10	52.6	19	6	BD016693 Method fo
4	10	52.6	19	6	E28797 Endoplasmic
5	10	52.6	19	6	E28801 Endoplasmic
6	10	52.6	19	6	E28802 Endoplasmic
7	10	52.6	19	6	E28803 Endoplasmic
8	10	52.6	19	6	E28804 Endoplasmic
9	10	52.6	19	6	E28805 Endoplasmic
10	10	52.6	19	6	E28806 Endoplasmic
11	10	52.6	19	6	E28807 Endoplasmic
12	10	52.6	19	6	E28808 Endoplasmic
13	10	52.6	19	6	E28809 Endoplasmic
14	10	52.6	19	6	E44202 Endoplasmic
15	10	52.6	19	6	E44206 Endoplasmic
16	10	52.6	19	6	E44207 Endoplasmic
17	10	52.6	19	6	E44208 Endoplasmic
18	10	52.6	19	6	E44209 Endoplasmic
19	10	52.6	19	6	E44210 Endoplasmic
20	10	52.6	19	6	E44211 Endoplasmic
21	10	52.6	19	6	E44212 Endoplasmic
22	10	52.6	19	6	E44213 Endoplasmic
23	10	52.6	19	6	E44214 Endoplasmic
24	10	52.6	24	6	AX443752 Sequence
25	10	52.6	25	6	AX447733 Sequence
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32	10	52.6	122	6	E28800 Endoplasmic
33	10	52.6	122	6	E44205 Endoplasmic
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35	10	52.6	127	6	AX343728 Sequence
36	10	52.6	133	8	ATH523697 Arabidops
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38	10	52.6	136	6	AX033516 Sequence
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40	10	52.6	142	6	AX033504 Sequence
41	10	52.6	143	6	AX033505 Sequence
42	10	52.6	143	9	D10339S05 Homo sapien
43	10	52.6	145	6	AX072778 Sequence
44	10	52.6	149	6	AX033508 Sequence
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ALIGNMENTS

RESULT 1	AR274677	Sequence 1 from patent US 6506600.	19 bp	DNA	linear	PAT 10-APR-2003
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DEFINITION	AR274677	Sequence 1 from patent US 6506600.	19 bp	DNA	linear	PAT 10-APR-2003
ACCESSION	AR274677	Sequence 1 from patent US 6506600.	19 bp	DNA	linear	PAT 10-APR-2003
VERSION	AR274677.1	GI:29707222	19 bp	DNA	linear	PAT 10-APR-2003
KEYWORDS	AR274677.1	GI:29707222	19 bp	DNA	linear	PAT 10-APR-2003
SOURCE	Unknown.	Unknown.	19 bp	DNA	linear	PAT 10-APR-2003
ORGANISM	Unknown.	Unknown.	19 bp	DNA	linear	PAT 10-APR-2003
REFERENCE	1 (bases 1 to 19)	Unknown.	19 bp	DNA	linear	PAT 10-APR-2003
AUTHORS	Hermonat, P.L., Mane, M. and Liu, Y.	Unknown.	19 bp	DNA	linear	PAT 10-APR-2003
TITLE	Secreting products from skin by adeno-associated virus (AAV) gene transfer	Unknown.	19 bp	DNA	linear	PAT 10-APR-2003
JOURNAL	Patent: US 6506600-A 1 14-JAN-2003;	Unknown.	19 bp	DNA	linear	PAT 10-APR-2003

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Db 1 CCAATNNNNNNNNCCACG 19

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LOCUS      AX275341      19 bp      DNA      linear      PAT 29-OCT-2001
DEFINITION Sequence 1 from Patent WO0171018.
ACCESSION  AX275341
VERSION     AX275341.1 GI:16547677
KEYWORDS
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1
AUTHORS     Hermonat,P.L., Mane,M. and Liu,Y.
TITLE       Secreting products from skin by adeno-associated virus (aav) gene transfer
JOURNAL     Patent: WO 0171018-A 1 27-SEP-2001;
            THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ARKANSAS (US)
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Db 1 CCAATNNNNNNNNCCACG 19

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LOCUS      BD016693      19 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Method for screening ORP150 expression regulatory substance.
ACCESSION  BD016693
VERSION     BD016693.1 GI:22557869
KEYWORDS    JP 2001238699-A/2.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Akazawa,R., Kaneda,S., Yanagi,H. and Yura,T.
TITLE       Method for screening ORP150 expression regulatory substance
JOURNAL     Patent: JP 2001238699-A 2 04-SEP-2001;
            HSP RESEARCH INST INC
COMMENT     OS Artificial Sequence
            PN JP 2001238699-A/2
            PD 04-SEP-2001
            PF 01-MAR-2000 JP 2000055384
            PI RIEKO AKAZAWA,SUMIKO KANEDA,HIDEKI YANAGI,TAKASHI YURA PC
            C12Q1/68,A61K45/00,A61P1/04,A61P9/10,A61P17/02,A61P25/ PC
            28,
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PC (C12N15/00,C12R1:91)
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS      E28797      19 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Endoplasmic reticulum stress-response regulatory element.
ACCESSION  E28797
VERSION     E28797.1 GI:13020851
KEYWORDS    JP 1999243959-A/1.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Hideo,Y., Hideki,Y. and Takashi,Y.
TITLE       Endoplasmic reticulum stress-response regulatory element
JOURNAL     Patent: JP 1999243959-A 1 14-SEP-1999;
            HSP RESEARCH INST INC
COMMENT     OS Unidentified
            PN JP 1999243959-A/1
            PD 14-SEP-1999
            PF 04-MAR-1998 JP 1998052453
            PI HIDEO YOSHIDA,HIDEKI YANAGI,TAKASHI YURA
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RESULT 5
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LOCUS      E28801      19 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Endoplasmic reticulum stress-response regulatory element.
ACCESSION  E28801
VERSION     E28801.1 GI:13020855
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KEYWORDS
SOURCE      JP 1999243959-A/5.
ORGANISM    Homo sapiens (human)

REFERENCE
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE       Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
JOURNAL     1 (bases 1 to 19)
            Hideo, Y., Hideki, Y. and Takashi, Y.
            Endoplasmic reticulum stress-response regulatory element
            Patent: JP 1999243959-A 5 14-SEP-1999;
            HSP RESEARCH INST INC

COMMENT     OS Homo sapiens (human)
            PN JP 1999243959-A/5
            PD 14-SEP-1999
            PF 04-MAR-1998 JP 1998052453
            PR HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
            PC C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
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Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 1 CCAATCGGAGGCTCCACG 19
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RESULT 7
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LOCUS      E28803
DEFINITION Endoplasmic reticulum stress-response regulatory element.
ACCESSION E28803
VERSION   E28803.1 GI:13020857
KEYWORDS  JP 1999243959-A/7.
SOURCE    Rattus sp.
ORGANISM  Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 19)
AUTHORS   Hideo, Y., Hideki, Y. and Takashi, Y.
TITLE     Endoplasmic reticulum stress-response regulatory element
JOURNAL   Patent: JP 1999243959-A 7 14-SEP-1999;
            HSP RESEARCH INST INC
COMMENT   OS Rattus sp. (rat)
            PN JP 1999243959-A/7
            PD 14-SEP-1999
            PF 04-MAR-1998 JP 1998052453
            PR HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
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LOCUS      E28804
DEFINITION Endoplasmic reticulum stress-response regulatory element.
ACCESSION E28804
VERSION   E28804.1 GI:13020858
KEYWORDS  JP 1999243959-A/8.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 19)
AUTHORS   Hideo, Y., Hideki, Y. and Takashi, Y.
TITLE     Endoplasmic reticulum stress-response regulatory element
JOURNAL   Patent: JP 1999243959-A 8 14-SEP-1999;
            HSP RESEARCH INST INC

KEYWORDS
SOURCE      JP 1999243959-A/5.
ORGANISM    Homo sapiens (human)

REFERENCE
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE       Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
JOURNAL     1 (bases 1 to 19)
            Hideo, Y., Hideki, Y. and Takashi, Y.
            Endoplasmic reticulum stress-response regulatory element
            Patent: JP 1999243959-A 5 14-SEP-1999;
            HSP RESEARCH INST INC

COMMENT     OS Homo sapiens (human)
            PN JP 1999243959-A/5
            PD 14-SEP-1999
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Db 1 CCAATCGGAGGCTCCACG 19
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DEFINITION Endoplasmic reticulum stress-response regulatory element.
ACCESSION E28802
VERSION   E28802.1 GI:13020856
KEYWORDS  JP 1999243959-A/6.
SOURCE    Mus sp.
ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 19)
            Hideo, Y., Hideki, Y. and Takashi, Y.
            Endoplasmic reticulum stress-response regulatory element
            Patent: JP 1999243959-A 6 14-SEP-1999;
            HSP RESEARCH INST INC
            OS Mus sp. (mouse)
            PN JP 1999243959-A/6
            PD 14-SEP-1999
            PF 04-MAR-1998 JP 1998052453
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COMMENT      OS Homo sapiens (human)
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RESULT 9
E28805 LOCUS 19 bp DNA linear PAT 18-JUN-2001
DEFINITION Endoplasmic reticulum stress-response regulatory element.
ACCESSION E28805
VERSION E28805.1 GI:13020859
KEYWORDS JP 1999243959-A/9.
SOURCE Gallus sp.
ORGANISM Gallus sp.

REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
              Phasianinae; Gallus.
AUTHORS Hideo,Y., Hideki,Y. and Takashi,Y.
TITLE Endoplasmic reticulum stress-response regulatory element
JOURNAL Patent: JP 1999243959-A 9 14-SEP-1999;
HSP RESEARCH INST INC
COMMENT OS Gallus sp. (chicken)
              PN JP 1999243959-A/9
              PD 14-SEP-1999
              PF 04-MAR-1998 JP 1998052453
              PR HIDEO YOSHIDA,HIDEKI YANAGI,TAKASHI YURA
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DEFINITION Endoplasmic reticulum stress-response regulatory element.
ACCESSION E28806
VERSION E28806.1 GI:13020860
KEYWORDS JP 1999243959-A/10.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Hideo,Y., Hideki,Y. and Takashi,Y.
TITLE Endoplasmic reticulum stress-response regulatory element
JOURNAL Patent: JP 1999243959-A 10 14-SEP-1999;
HSP RESEARCH INST INC
COMMENT OS Homo sapiens (human)
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DEFINITION Endoplasmic reticulum stress-response regulatory element.
ACCESSION E28807
VERSION E28807.1 GI:13020861
KEYWORDS JP 1999243959-A/11.
SOURCE Gallus sp.
ORGANISM Gallus sp.

REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
              Phasianinae; Gallus.
AUTHORS Hideo,Y., Hideki,Y. and Takashi,Y.
TITLE Endoplasmic reticulum stress-response regulatory element
JOURNAL Patent: JP 1999243959-A 11 14-SEP-1999;
HSP RESEARCH INST INC
COMMENT OS Gallus sp. (chicken)
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              PD 14-SEP-1999
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RESULT 12  
E28808  
LOCUS E28808 19 bp DNA linear PAT 18-JUN-2001  
DEFINITION Endoplasmic reticulum stress-response regulatory element.  
ACCESSION E28808  
VERSION E28808.1 GI:13020862  
KEYWORDS JP 1999243959-A/12.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
Hideo,Y., Hideki,Y. and Takashi,Y.  
Endoplasmic reticulum stress-response regulatory element  
Patent: JP 1999243959-A 12-SEP-1999;  
HSP RESEARCH INST INC  
OS Homo sapiens (human)  
PN JP 1999243959-A/12  
PD 14-SEP-1999  
PF 04-MAR-1998 JP 1998052453  
PR HIDEO YOSHIDA,HIDEKI YANAGI,TAKASHI YURA  
PC C12N15/09,A61K35/74,A61K38/00,A61K48/00,C12N15/00,  
A61K37/02  
CC Strandedness: Double;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
FT enhancer 1..19.  
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Best Local Similarity 52.6%; Pred. No. 2.7e+04;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
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Db 1 CCAATGATGTCGACCACG 19  
RESULT 13  
E28809  
LOCUS E28809 19 bp DNA linear PAT 18-JUN-2001  
DEFINITION Endoplasmic reticulum stress-response regulatory element.  
ACCESSION E28809  
VERSION E28809.1 GI:13020863  
KEYWORDS JP 1999243959-A/13.  
SOURCE Mus sp.

ORGANISM Mus sp.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Hideo,Y., Hideki,Y. and Takashi,Y.  
Endoplasmic reticulum stress-response regulatory element  
Patent: JP 1999243959-A 13-SEP-1999;  
HSP RESEARCH INST INC  
OS Mus sp. (mouse)  
PN JP 1999243959-A/13  
PD 14-SEP-1999  
PF 04-MAR-1998 JP 1998052453  
PR HIDEO YOSHIDA,HIDEKI YANAGI,TAKASHI YURA  
PC C12N15/09,A61K35/74,A61K38/00,A61K48/00,C12N15/00,  
A61K37/02  
CC Strandedness: Double;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
FT enhancer 1..19.  
Location/Qualifiers  
1..19  
/organism="Mus sp."  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10095" 2 t  
BASE COUNT 5 a 6 c 6 g 2 t  
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Best Local Similarity 52.6%; Pred. No. 2.7e+04;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
Qy 1 CCAATNNNNNNNCCACG 19  
Db 1 CCAATGAGGTCGACCACG 19  
RESULT 14  
E44202  
LOCUS E44202 19 bp DNA linear PAT 31-JAN-2002  
DEFINITION Endoplasmic reticulum stress transcription factor.  
ACCESSION E44202  
VERSION E44202.1 GI:18633455  
KEYWORDS JP 2001054391-A/1.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
1 (bases 1 to 19)  
Haji,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.  
Endoplasmic reticulum stress transcription factor  
Patent: JP 2001054391-A 1-27-FEB-2001;  
HSP RESEARCH INST INC  
OS Artificial Sequence  
PN JP 2001054391-A/1  
PD 27-FEB-2001  
PF 11-NOV-1999 JP 1999321743  
PR KYOSUKE HAJI,HIDEO YOSHIDA,KAZUTOSHI MORI,HIDEKI YANAGI, PI  
TAKASHI YURA  
PC C12N15/09,C12P21/02//(C12N15/09,C12R1:91),C12N15/00,(C12N15/00,PC  
C12R1:91)  
CC  
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Location/Qualifiers  
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/organism="synthetic construct"  
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Best Local Similarity 100.0%; Pred. No. 2.7e+04;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNCCACG 19  
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Db 1 CCAATNNNNNNNCCACG 19

RESULT 15  
E44206  
LOCUS E44206 19 bp DNA linear PAT 31-JAN-2002  
DEFINITION Endoplasmic reticulum stress transcription factor.  
ACCESSION E44206  
VERSION E44206.1 GI:18633459  
KEYWORDS JP 2001054391-A/5.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
Hajj, K., Yoshida, H., Mori, K., Yanagi, H. and Yura, T.  
Endoplasmic reticulum stress transcription factor  
Patent: JP 2001054391-A 5 27-FEB-2001;  
HSP RESEARCH INST INC  
OS Homo sapiens (human)  
PN JP 2001054391-A/5  
PD 27-FEB-2001  
PF 11-NOV-1999 JP 1999321743

PI KYOSUKE HAJI, HIDEO YOSHIDA, KAZUTOSHI MORI, HIDEKI YANAGI, PI  
TAKASHI YURA  
PC  
C12N15/09, C12P21/02// (C12N15/09, C12R1:91), C12N15/00, (C12N15/00, PC  
C12R1:91)  
CC  
FH Key Location/Qualifiers  
FT source 1..19 /organism='Homo sapiens (human)'.  
FEATURES  
source Location/Qualifiers  
1..19  
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/db\_xref="taxon:9606"

BASE COUNT 3 a 9 c 5 g 2 t  
ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;  
Best Local Similarity 52.6%; Pred. No. 2.7e+04;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNCCACG 19  
|||||  
Db 1 CCAATCGGCGCTCCACG 19

Search completed: December 4, 2003, 09:21:23  
Job time : 1501 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 07:47:59 ; Search time 261 Seconds  
(without alignments)  
196.511 Million cell updates/sec

Title: US-09-606-804-1

Perfect score: 19  
Sequence: 1 ccaatnnnnnnnccacg 19

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	52.6	19	AAZ25631	Endoplasmic reticu
2	10	52.6	19	AAZ25632	Endoplasmic reticu
3	10	52.6	19	AAZ25633	Endoplasmic reticu
4	10	52.6	19	AAZ25634	Endoplasmic reticu
5	10	52.6	19	AAZ25635	Endoplasmic reticu
6	10	52.6	19	AAZ25636	Endoplasmic reticu
7	10	52.6	19	AAZ25637	Endoplasmic reticu
8	10	52.6	19	AAZ25638	Endoplasmic reticu

9	10	52.6	19	20	AAZ25639	Endoplasmic reticu
10	10	52.6	19	20	AAZ25640	Endoplasmic reticu
11	10	52.6	19	21	AAA28570	GRP78 promoter ERS
12	10	52.6	19	21	AAA28571	GRP78 promoter ERS
13	10	52.6	19	21	AAA28572	GRP78 promoter ERS
14	10	52.6	19	21	AAA28573	GRP94 promoter ERS
15	10	52.6	19	21	AAA28574	GRP94 promoter ERS
16	10	52.6	19	21	AAA28575	GRP94 promoter ERS
17	10	52.6	19	21	AAA28576	GRP94 promoter ERS
18	10	52.6	19	21	AAA28577	GRP94 promoter ERS
19	10	52.6	19	21	AAA28578	Calreticulin promo
20	10	52.6	19	21	AAA28579	Calreticulin promo
21	10	52.6	19	22	AAI70001	ERSE consensus se
22	10	52.6	19	22	AAI70002	ERSE consensus se
23	10	52.6	19	22	AAI70003	ERSE consensus se
24	10	52.6	19	22	AAI70004	ERSE consensus se
25	10	52.6	19	22	AAI70005	ERSE consensus se
26	10	52.6	19	22	AAI70006	ERSE consensus se
27	10	52.6	19	22	AAI70007	ERSE consensus se
28	10	52.6	19	22	AAI70008	ERSE consensus se
29	10	52.6	19	22	AAI70009	ERSE consensus se
30	10	52.6	19	22	AAI70010	ERSE consensus se
31	10	52.6	19	22	AAI70011	ERSE consensus se
32	10	52.6	19	22	AAI70012	ERSE consensus se
33	10	52.6	19	22	AAI70013	ERSE consensus se
34	10	52.6	19	22	AAI70014	ERSE consensus se
35	10	52.6	19	22	AAI70015	ERSE consensus se
36	10	52.6	19	22	AAI70016	ERSE consensus se
37	10	52.6	19	22	AAI70017	ERSE consensus se
38	10	52.6	19	22	AAI70018	ERSE consensus se
39	10	52.6	19	22	AAI70019	ERSE consensus se
40	10	52.6	19	22	AAI70020	ERSE consensus se
41	10	52.6	19	22	AAI70021	ERSE consensus se
42	10	52.6	19	22	AAI70022	ERSE consensus se
43	10	52.6	19	22	AAI70023	ERSE consensus se
44	10	52.6	19	22	AAI70024	ERSE consensus se
45	10	52.6	19	22	AAI70025	ERSE consensus se

#### ALIGNMENTS

RESULT 1  
AAZ25631  
ID AAZ25631 standard; DNA; 19 BP.  
XX AAZ25631;  
AC AAZ25631;  
XX  
DT 23-DEC-1999 (first entry)  
XX  
DE Endoplasmic reticulum stress competence control element SEQ ID NO:1.  
XX  
KW Endoplasmic reticulum; ER; stress competence; control element;  
KW inhibition; growth; apoptosis; cancer; autoimmune disease;  
KW cystic fibrosis; da.  
XX  
OS Homo sapiens.  
XX  
PN JP1243959-A.  
XX  
PD 14-SEP-1999.  
XX  
PF 04-MAR-1998; 98JP-0052453.  
XX  
PR 04-MAR-1998; 98JP-0052453.  
XX  
PA (HSPK-) HSP KENKYUSHO KK.  
XX  
DR WPI; 1999-603708/52.  
XX  
PT New control element for stress competence of endoplasmic reticulum -  
PT useful for inhibition of growth and induction of apoptosis in cancer  
PT cells

```
XX PS Claim 1; Page 10; 25pp; Japanese.
XX CC The present invention specifically claims an element shown by: (A) a
CC 19 bp base sequence, CCAATNNNN NNNCCACG (ERSE); or (B) a modified base
CC sequence having replaced 1-3 bases with the other base(s), which induces
CC transcriptions with stress on endoplasmic reticulum used for stress
CC competence of endoplasmic reticulum. Also described are: (1) a DNA having
CC transcriptions inducing activity with stress on endoplasmic reticulum
CC containing the above mentioned element, optionally further containing a
CC promoter DNA; and (2) a vector containing the element optionally with the
CC DNA. The element can be used for the inhibition of growth and induction
CC of apoptosis of cancer cells, and improvement of symptoms of autoimmune
CC diseases and cystic fibrosis by inhibition of autoantibody formation.
XX SQ Sequence 19 BP; 3 A; 5 C; 1 G; 1 T; 9 other;

Query Match 52.6%; Score 10; DB 20; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
DB 1 CCAATNNNNNNNNCCACG 19
|||||
|||||

RESULT 2
AAZ25632
ID .AAZ25632 standard; DNA; 19 BP.
XX AC AAZ25632;
XX DT 23-DEC-1999 (first entry)
XX DE Endoplasmic reticulum stress competence control element SEQ ID NO:5.
XX KW Endoplasmic reticulum; ER; stress competence; control element;
XX KW inhibition; growth; apoptosis; cancer; autoimmune disease;
XX KW cystic fibrosis; ds.
XX OS Homo sapiens.
XX PN JP11243959-A.
XX PD 14-SEP-1999.
XX PF 04-MAR-1998; 98JP-0052453.
XX PR 04-MAR-1998; 98JP-0052453.
XX PA (HSPK-) HSP KENKYUSHO KK.
XX DR WPI; 1999-603708/52.
XX PT New control element for stress competence of endoplasmic reticulum -
XX PT useful for inhibition of growth and induction of apoptosis in cancer
XX PS cells
XX PS Example 1; Fig 3; 25pp; Japanese.
XX CC The present invention specifically claims an element shown by: (A) a
XX CC 19 bp base sequence, CCAATNNNN NNNCCACG (ERSE); or (B) a modified base
XX CC sequence having replaced 1-3 bases with the other base(s), which induces
XX CC transcriptions with stress on endoplasmic reticulum used for stress
XX CC competence of endoplasmic reticulum. Also described are: (1) a DNA
XX CC having transcriptions inducing activity with stress on endoplasmic
XX CC reticulum containing the above mentioned element, optionally further
XX CC containing a promoter DNA; and (2) a vector containing the element
XX CC optionally with the DNA. The element can be used for the inhibition of
XX CC growth and induction of apoptosis of cancer cells, and improvement of
XX CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
XX CC autoantibody formation. AAZ25632 to AAZ25657 represent elements used in
XX CC an example from the present invention.

Query Match 52.6%; Score 10; DB 20; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
DB 1 CCAATNNNNNNNNCCACG 19
|||||
|||||

RESULT 3
AAZ25633
ID .AAZ25633 standard; DNA; 19 BP.
XX AC AAZ25633;
XX DT 23-DEC-1999 (first entry)
XX DE Endoplasmic reticulum stress competence control element SEQ ID NO:6.
XX KW Endoplasmic reticulum; ER; stress competence; control element;
XX KW inhibition; growth; apoptosis; cancer; autoimmune disease;
XX KW cystic fibrosis; ds.
XX OS Mus sp.
XX PN JP11243959-A.
XX PD 14-SEP-1999.
XX PF 04-MAR-1998; 98JP-0052453.
XX PR 04-MAR-1998; 98JP-0052453.
XX PA (HSPK-) HSP KENKYUSHO KK.
XX DR WPI; 1999-603708/52.
XX PT New control element for stress competence of endoplasmic reticulum -
XX PT useful for inhibition of growth and induction of apoptosis in cancer
XX PS cells
XX PS Example 1; Fig 3; 25pp; Japanese.
XX CC The present invention specifically claims an element shown by: (A) a
XX CC 19 bp base sequence, CCAATNNNN NNNCCACG (ERSE); or (B) a modified base
XX CC sequence having replaced 1-3 bases with the other base(s), which induces
XX CC transcriptions with stress on endoplasmic reticulum used for stress
XX CC competence of endoplasmic reticulum. Also described are: (1) a DNA
XX CC having transcriptions inducing activity with stress on endoplasmic
XX CC reticulum containing the above mentioned element, optionally further
XX CC containing a promoter DNA; and (2) a vector containing the element
XX CC optionally with the DNA. The element can be used for the inhibition of
XX CC growth and induction of apoptosis of cancer cells, and improvement of
XX CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
XX CC autoantibody formation. AAZ25632 to AAZ25657 represent elements used in
XX CC an example from the present invention.

Query Match 52.6%; Score 10; DB 20; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
DB 1 CCAATCGGCGCCTCCACG 19
|||||
|||||

RESULT 4
AAZ25634
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ID AA225634 standard; DNA; 19 BP.
XX AC AA225634;
XX DT 23-DEC-1999 (first entry)
XX DE Endoplasmic reticulum stress competence control element SEQ ID NO:7.
XX KW Endoplasmic reticulum; ER; stress competence; control element;
XX KW inhibition; growth; apoptosis; cancer; autoimmune disease;
XX KW cystic fibrosis; ds.
XX OS Rattus sp.
XX PN JP11243959-A.
XX PD 14-SEP-1999.
XX PF 04-MAR-1998; 98JP-0052453.
XX PR 04-MAR-1998; 98JP-0052453.
XX PA (HSPK-) HSP KENKYUSHO KK.
XX DR WPI; 1999-603708/52.
XX PT New control element for stress competence of endoplasmic reticulum -
XX PT useful for inhibition of growth and induction of apoptosis in cancer
XX PS cells
XX PS Example 1; Fig 3; 25pp; Japanese.
XX CC The present invention specifically claims an element shown by: (A) a
XX CC 19 bp base sequence, CCAATNNNNN NNNCCACG (ERSE); or (B) a modified base
XX CC sequence having replaced 1-3 bases with the other base(s), which induces
XX CC transcription with stress on endoplasmic reticulum used for stress
XX CC competence of endoplasmic reticulum. Also described are: (1) a DNA
XX CC having transcription inducing activity with stress on endoplasmic
XX CC reticulum containing the above mentioned element, optionally further
XX CC containing a promoter DNA; and (2) a vector containing the element
XX CC optionally with the DNA. The element can be used for the inhibition of
XX CC growth and induction of apoptosis of cancer cells, and improvement of
XX CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
XX CC autoantibody formation. AA225632 to AA225657 represent elements used in
XX CC an example from the present invention.
XX SQ Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other;

Query Match 52.6%; Score 10; DB 20; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNN NNNCCACG 19
Db 1 CCAATCGGAGCTCCACG 19

RESULT 5
AA225635
ID AA225635 standard; DNA; 19 BP.
XX AC AA225635;
XX DT 23-DEC-1999 (first entry)
XX DE Endoplasmic reticulum stress competence control element SEQ ID NO:8.
XX KW Endoplasmic reticulum; ER; stress competence; control element;
XX KW inhibition; growth; apoptosis; cancer; autoimmune disease;
XX KW cystic fibrosis; ds.
XX OS Homo sapiens.
XX PT New control element for stress competence of endoplasmic reticulum -
XX PT useful for inhibition of growth and induction of apoptosis in cancer

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PN JP11243959-A.
XX PD 14-SEP-1999.
XX PF 04-MAR-1998; 98JP-0052453.
XX PR 04-MAR-1998; 98JP-0052453.
XX PA (HSPK-) HSP KENKYUSHO KK.
XX DR WPI; 1999-603708/52.
XX PT New control element for stress competence of endoplasmic reticulum -
XX PT useful for inhibition of growth and induction of apoptosis in cancer
XX PS cells
XX PS Example 1; Fig 3; 25pp; Japanese.
XX CC The present invention specifically claims an element shown by: (A) a
XX CC 19 bp base sequence, CCAATNNNNN NNNCCACG (ERSE); or (B) a modified base
XX CC sequence having replaced 1-3 bases with the other base(s), which induces
XX CC transcription with stress on endoplasmic reticulum used for stress
XX CC competence of endoplasmic reticulum. Also described are: (1) a DNA
XX CC having transcription inducing activity with stress on endoplasmic
XX CC reticulum containing the above mentioned element, optionally further
XX CC containing a promoter DNA; and (2) a vector containing the element
XX CC optionally with the DNA. The element can be used for the inhibition of
XX CC growth and induction of apoptosis of cancer cells, and improvement of
XX CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
XX CC autoantibody formation. AA225632 to AA225657 represent elements used in
XX CC an example from the present invention.
XX SQ Sequence 19 BP; 4 A; 10 C; 4 G; 1 T; 0 other;

Query Match 52.6%; Score 10; DB 20; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNN NNNCCACG 19
Db 1 CCAATCGGCGGCACACG 19

RESULT 6
AA225636
ID AA225636 standard; DNA; 19 BP.
XX AC AA225636;
XX DT 23-DEC-1999 (first entry)
XX DE Endoplasmic reticulum stress competence control element SEQ ID NO:9.
XX KW Endoplasmic reticulum; ER; stress competence; control element;
XX KW inhibition; growth; apoptosis; cancer; autoimmune disease;
XX KW cystic fibrosis; ds.
XX OS Gallus sp.
XX PN JP11243959-A.
XX PD 14-SEP-1999.
XX PF 04-MAR-1998; 98JP-0052453.
XX PR 04-MAR-1998; 98JP-0052453.
XX PA (HSPK-) HSP KENKYUSHO KK.
XX DR WPI; 1999-603708/52.
XX PT New control element for stress competence of endoplasmic reticulum -
XX PT useful for inhibition of growth and induction of apoptosis in cancer

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PT cells
PS Example 1; Fig 3; 25pp; Japanese.
XX
CC The present invention specifically claims an element shown by: (A) a
CC 19 bp base sequence, CCAATNNNN NNNCCACG (ERSE); or (B) a modified base
CC sequence having replaced 1-3 bases with the other base(s), which induces
CC transcriptions with stress on endoplasmic reticulum used for stress
CC competence of endoplasmic reticulum. Also described are: (1) a DNA
CC having transcription inducing activity with stress on endoplasmic
CC reticulum containing the above mentioned element, optionally further
CC containing a promoter DNA; and (2) a vector containing the element
CC optionally with the DNA. The element can be used for the inhibition of
CC growth and induction of apoptosis of cancer cells, and improvement of
CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
CC autoantibody formation. AA225632 to AA225657 represent elements used in
CC an example from the present invention.
XX
SQ Sequence 19 BP; 5 A; 7 C; 6 G; 1 T; 0 other;
    Query Match          52.6%; Score 10; DB 20; Length 19;
    Best Local Similarity 52.6%; Pred. No. 1.8e+03;
    Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
Db 1 CCAATGGGAGCGCACCCACG 19

RESULT 7
AA225637
ID AA225637 standard; DNA; 19 BP.
XX
AC AA225637;
XX
DT 23-DEC-1999 (first entry)
XX
DE Endoplasmic reticulum stress competence control element SEQ ID NO:10.
XX
KW Endoplasmic reticulum; ER; stress competence; control element;
KW inhibition; growth; apoptosis; cancer; autoimmune disease;
KW cystic fibrosis; ds.
XX
OS Homo sapiens.
XX
PN JP11243959-A.
XX
PD 14-SEP-1999.
XX
PF 04-MAR-1998; 98JP-0052453.
XX
PR 04-MAR-1998; 98JP-0052453.
XX
PA (HSPK-) HSP KENKYUSHO KK.
XX
DR WPI; 1999-603708/52.
XX
PT New control element for stress competence of endoplasmic reticulum -
PT useful for inhibition of growth and induction of apoptosis in cancer
PT cells
PS Example 1; Fig 3; 25pp; Japanese.
XX
CC The present invention specifically claims an element shown by: (A) a
CC 19 bp base sequence, CCAATNNNN NNNCCACG (ERSE); or (B) a modified base
CC sequence having replaced 1-3 bases with the other base(s), which induces
CC transcriptions with stress on endoplasmic reticulum used for stress
CC competence of endoplasmic reticulum. Also described are: (1) a DNA
CC having transcription inducing activity with stress on endoplasmic
CC reticulum containing the above mentioned element, optionally further
CC containing a promoter DNA; and (2) a vector containing the element
CC optionally with the DNA. The element can be used for the inhibition of
CC growth and induction of apoptosis of cancer cells, and improvement of
CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
CC autoantibody formation. AA225632 to AA225657 represent elements used in
CC an example from the present invention.
XX
SQ Sequence 19 BP; 5 A; 7 C; 6 G; 1 T; 0 other;
    Query Match          52.6%; Score 10; DB 20; Length 19;
    Best Local Similarity 52.6%; Pred. No. 1.8e+03;
    Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
Db 1 CCAATGGGAGCGCACCCACG 19

RESULT 8
AA225638
ID AA225638 standard; DNA; 19 BP.
XX
AC AA225638;
XX
DT 23-DEC-1999 (first entry)
XX
DE Endoplasmic reticulum stress competence control element SEQ ID NO:11.
XX
KW Endoplasmic reticulum; ER; stress competence; control element;
KW inhibition; growth; apoptosis; cancer; autoimmune disease;
KW cystic fibrosis; ds.
XX
OS Gallus sp.
XX
PN JP11243959-A.
XX
PD 14-SEP-1999.
XX
PF 04-MAR-1998; 98JP-0052453.
XX
PR 04-MAR-1998; 98JP-0052453.
XX
PA (HSPK-) HSP KENKYUSHO KK.
XX
DR WPI; 1999-603708/52.
XX
PT New control element for stress competence of endoplasmic reticulum -
PT useful for inhibition of growth and induction of apoptosis in cancer
PT cells
PS Example 1; Fig 3; 25pp; Japanese.
XX
CC The present invention specifically claims an element shown by: (A) a
CC 19 bp base sequence, CCAATNNNN NNNCCACG (ERSE); or (B) a modified base
CC sequence having replaced 1-3 bases with the other base(s), which induces
CC transcriptions with stress on endoplasmic reticulum used for stress
CC competence of endoplasmic reticulum. Also described are: (1) a DNA
CC having transcription inducing activity with stress on endoplasmic
CC reticulum containing the above mentioned element, optionally further
CC containing a promoter DNA; and (2) a vector containing the element
CC optionally with the DNA. The element can be used for the inhibition of
CC growth and induction of apoptosis of cancer cells, and improvement of
CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
CC autoantibody formation. AA225632 to AA225657 represent elements used in
CC an example from the present invention.
XX
SQ Sequence 19 BP; 4 A; 9 C; 5 G; 1 T; 0 other;
    Query Match          52.6%; Score 10; DB 20; Length 19;
    Best Local Similarity 52.6%; Pred. No. 1.8e+03;
    Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
Db 1 CCAATCGACGCGCGCACG 19

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RESULT 9
AAZ25639
ID AAZ25639 standard; DNA; 19 BP.
XX
XX AAZ25639;
AC
DT 23-DEC-1999 (first entry)
XX
XX Endoplasmic reticulum stress competence control element SEQ ID NO:12.
DE
XX Endoplasmic reticulum; ER; stress competence; control element;
KW inhibition; growth; apoptosis; cancer; autoimmune disease;
KW cystic fibrosis; ds.
XX
XX Homo sapiens.
OS
XX JPI1243959-A.
XX
XX 14-SEP-1999.
PD
XX
XX 04-MAR-1998; 98JJP-0052453.
PF
XX
XX 04-MAR-1998; 98JJP-0052453.
PR
XX (HSPK-) HSP KENKYUSHO KK.
PA
XX WPI; 1999-603708/52.
DR
XX
XX New control element for stress competence of endoplasmic reticulum -
PT useful for inhibition of growth and induction of apoptosis in cancer
PT cells
XX
XX Example 1; Fig 3; 25pp; Japanese.
PS
XX The present invention specifically claims an element shown by: (A) a
CC 19 bp base sequence, CCAATNNNNN NNNCCACG (ERSE); or (B) a modified base
CC sequence having replaced 1-3 bases with the other base(s), which induces
CC transcription with stress on endoplasmic reticulum used for stress
CC competence of endoplasmic reticulum. Also described are: (1) a DNA
CC having transcription inducing activity with stress on endoplasmic
CC reticulum containing the above mentioned element, optionally further
CC containing a promoter DNA; and (2) a vector containing the element
CC optionally with the DNA. The element can be used for the inhibition of
CC growth and induction of apoptosis of cancer cells, and improvement of
CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
CC autoantibody formation. AAZ25632 to AAZ25657 represent elements used in
CC an example from the present invention.
XX
XX Sequence 19 BP; 5 A; 6 C; 5 G; 3 T; 0 other;
SQ
Query Match 52.6%; Score 10; DB 20; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNN NNNCCACG 19
    |||||
Db 1 CCAATGATGTCGACCACG 19
    |||||

RESULT 10
AAZ25640
ID AAZ25640 standard; DNA; 19 BP.
XX
XX AAZ25640;
AC
DT 23-DEC-1999 (first entry)
XX
XX Endoplasmic reticulum stress competence control element SEQ ID NO:13.
DE
XX Endoplasmic reticulum; ER; stress competence; control element;
KW inhibition; growth; apoptosis; cancer; autoimmune disease;
KW cystic fibrosis; ds.
XX
XX Homo sapiens.
OS
XX JPI1243959-A.
XX
XX 14-SEP-1999.
PD
XX
XX 04-MAR-1998; 98JJP-0052453.
PF
XX
XX 04-MAR-1998; 98JJP-0052453.
PR
XX (HSPK-) HSP KENKYUSHO KK.
PA
XX WPI; 1999-603708/52.
DR
XX
XX New control element for stress competence of endoplasmic reticulum -
PT useful for inhibition of growth and induction of apoptosis in cancer
PT cells
XX
XX Example 1; Fig 3; 25pp; Japanese.
PS
XX The present invention specifically claims an element shown by: (A) a
CC 19 bp base sequence, CCAATNNNNN NNNCCACG (ERSE); or (B) a modified base
CC sequence having replaced 1-3 bases with the other base(s), which induces
CC transcription with stress on endoplasmic reticulum used for stress
CC competence of endoplasmic reticulum. Also described are: (1) a DNA
CC having transcription inducing activity with stress on endoplasmic
CC reticulum containing the above mentioned element, optionally further
CC containing a promoter DNA; and (2) a vector containing the element
CC optionally with the DNA. The element can be used for the inhibition of
CC growth and induction of apoptosis of cancer cells, and improvement of
CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
CC autoantibody formation. AAZ25632 to AAZ25657 represent elements used in
CC an example from the present invention.
XX
XX Sequence 19 BP; 5 A; 6 C; 5 G; 3 T; 0 other;
SQ
Query Match 52.6%; Score 10; DB 20; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNN NNNCCACG 19
    |||||
Db 1 CCAATGATGTCGACCACG 19
    |||||

RESULT 11
AAA28570
ID AAA28570 standard; DNA; 19 BP.
XX
XX AAA28570;
AC
DT 29-AUG-2000 (first entry)
XX
XX GRP78 promoter ERSE1-like sequence.
DE
XX Endoplasmic reticulum; stress; ER; transcription factor;
KW transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
KW prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing;
KW cystic fibrosis; ulcer; gene therapy; recombinant gene; human;
KW gene expression; GRP; glucose regulated protein; promoter; ss.
XX
XX Homo sapiens.
OS
XX WO200029429-A2.
XX
XX 25-MAY-2000.
PD
XX
XX 12-NOV-1999; 99WO-JP06305.
PF
XX
XX 13-NOV-1998; 98JP-0324227.
PR
XX 09-JUN-1999; 99JP-0163112.
XX

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XX Mus sp.
OS
XX JPI1243959-A.
XX
XX 14-SEP-1999.
PD
XX
XX 04-MAR-1998; 98JJP-0052453.
PF
XX
XX 04-MAR-1998; 98JJP-0052453.
PR
XX (HSPK-) HSP KENKYUSHO KK.
PA
XX WPI; 1999-603708/52.
DR
XX
XX New control element for stress competence of endoplasmic reticulum -
PT useful for inhibition of growth and induction of apoptosis in cancer
PT cells
XX
XX Example 1; Fig 3; 25pp; Japanese.
PS
XX The present invention specifically claims an element shown by: (A) a
CC 19 bp base sequence, CCAATNNNNN NNNCCACG (ERSE); or (B) a modified base
CC sequence having replaced 1-3 bases with the other base(s), which induces
CC transcription with stress on endoplasmic reticulum used for stress
CC competence of endoplasmic reticulum. Also described are: (1) a DNA
CC having transcription inducing activity with stress on endoplasmic
CC reticulum containing the above mentioned element, optionally further
CC containing a promoter DNA; and (2) a vector containing the element
CC optionally with the DNA. The element can be used for the inhibition of
CC growth and induction of apoptosis of cancer cells, and improvement of
CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
CC autoantibody formation. AAZ25632 to AAZ25657 represent elements used in
CC an example from the present invention.
XX
XX Sequence 19 BP; 5 A; 6 C; 6 G; 2 T; 0 other;
SQ
Query Match 52.6%; Score 10; DB 20; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNN NNNCCACG 19
    |||||
Db 1 CCAATGAGGTCGACCACG 19
    |||||

RESULT 11
AAA28570
ID AAA28570 standard; DNA; 19 BP.
XX
XX AAA28570;
AC
DT 29-AUG-2000 (first entry)
XX
XX GRP78 promoter ERSE1-like sequence.
DE
XX Endoplasmic reticulum; stress; ER; transcription factor;
KW transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
KW prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing;
KW cystic fibrosis; ulcer; gene therapy; recombinant gene; human;
KW gene expression; GRP; glucose regulated protein; promoter; ss.
XX
XX Homo sapiens.
OS
XX WO200029429-A2.
XX
XX 25-MAY-2000.
PD
XX
XX 12-NOV-1999; 99WO-JP06305.
PF
XX
XX 13-NOV-1998; 98JP-0324227.
PR
XX 09-JUN-1999; 99JP-0163112.
XX

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PA (HSPR-) HSP RES INST INC.
PI Haze K, Yoshida H, Mori K, Yanagi H, Yura T;
XX WPI; 2000-387736/33.
XX
XX New endoplasmic reticulum stress transcription factor (known as bZIP)
PT for controlling expression of endoplasmic reticulum chaperone, useful
PT for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
PT diseases, wounds and ulcers
XX
XX Example 1; Fig 3; 157pp; English.
XX
XX An endoplasmic reticulum stress transcription factor (bZIP)
CC capable of regulating transcription inducing activity exhibited by an
CC element (ERSE) can be used in a method for controlling expression of
CC an endoplasmic reticulum chaperone. The method comprises expressing
CC bZIP. The method can be used for expression of a foreign protein by
CC positively regulating expression of an endoplasmic reticulum
CC chaperone gene. bZIP is useful for controlling the expression of
CC endoplasmic reticulum chaperone either positively or negatively in
CC cells and therefore is useful for treatment or prophylaxis of
CC cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases,
CC wounds and ulcers. bZIP also maintains the correct conformation of
CC the endoplasmic reticulum chaperone and thereby increases the
CC expression of a foreign protein. This sequence taken from the
CC glucose regulating protein (GRP) promoter GRP78 contains an ERSE like
CC sequence.
XX
SQ Sequence 19 BP; 3 A; 9 C; 5 G; 2 T; 0 other;
Query Match 52.6%; Score 10; DB 21; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
Db ||||| |||||
1 CCAATCGGCGCTCCACG 19

RESULT 12
AAA28571
ID AAA28571 standard; DNA; 19 BP.
XX
AC AAA28571;
XX
DT 29-AUG-2000 (first entry)
XX
DE GRP78 promoter ERSE1-like sequence.
XX
KW Endoplasmic reticulum; stress; ER; transcription factor;
KW transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
KW prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing;
KW cystic fibrosis; ulcer; gene therapy; recombinant gene; mouse;
KW gene expression; GRP; glucose regulated protein; promoter; ss.
XX
OS Mus musculus.
XX
PN WO200029429-A2.
XX
XX 25-MAY-2000.
XX
PF 12-NOV-1999; 99WO-JP06305.
XX
PR 13-NOV-1998; 98JP-0324227.
XX
PR 09-JUN-1999; 99JP-0163112.
XX
PA (HSPR-) HSP RES INST INC.
XX
PI Haze K, Yoshida H, Mori K, Yanagi H, Yura T;
XX WPI; 2000-387736/33.
XX

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PT New endoplasmic reticulum stress transcription factor (known as bZIP)
PT for controlling expression of endoplasmic reticulum chaperone, useful
PT for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
PT diseases, wounds and ulcers
XX
XX Example 1; Fig 3; 157pp; English.
XX
XX An endoplasmic reticulum stress transcription factor (bZIP)
CC capable of regulating transcription inducing activity exhibited by an
CC element (ERSE) can be used in a method for controlling expression of
CC an endoplasmic reticulum chaperone. The method comprises expressing
CC bZIP. The method can be used for expression of a foreign protein by
CC positively regulating expression of an endoplasmic reticulum
CC chaperone gene. bZIP is useful for controlling the expression of
CC endoplasmic reticulum chaperone either positively or negatively in
CC cells and therefore is useful for treatment or prophylaxis of
CC cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases,
CC wounds and ulcers. bZIP also maintains the correct conformation of
CC the endoplasmic reticulum chaperone and thereby increases the
CC expression of a foreign protein. This sequence taken from the
CC glucose regulating protein (GRP) promoter GRP78 contains an ERSE like
CC sequence.
XX
SQ Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other;
Query Match 52.6%; Score 10; DB 21; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
Db ||||| |||||
1 CCAATCGGCGCTCCACG 19

RESULT 13
AAA28572
ID AAA28572 standard; DNA; 19 BP.
XX
AC AAA28572;
XX
DT 29-AUG-2000 (first entry)
XX
DE GRP78 promoter ERSE1-like sequence.
XX
KW Endoplasmic reticulum; stress; ER; transcription factor;
KW transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
KW prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing;
KW cystic fibrosis; ulcer; gene therapy; recombinant gene; rat;
KW gene expression; GRP; glucose regulated protein; promoter; ss.
XX
OS Rattus rattus.
XX
PN WO200029429-A2.
XX
XX 25-MAY-2000.
XX
PF 12-NOV-1999; 99WO-JP06305.
XX
PR 13-NOV-1998; 98JP-0324227.
XX
PR 09-JUN-1999; 99JP-0163112.
XX
PA (HSPR-) HSP RES INST INC.
XX
XX Haze K, Yoshida H, Mori K, Yanagi H, Yura T;
XX WPI; 2000-387736/33.
XX
XX New endoplasmic reticulum stress transcription factor (known as bZIP)
PT for controlling expression of endoplasmic reticulum chaperone, useful
PT for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
PT diseases, wounds and ulcers
XX
XX Example 1; Fig 3; 157pp; English.
XX

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XX CC An endoplasmic reticulum stress transcription factor (bZIP)
CC capable of regulating transcription inducing activity exhibited by an
CC element (ERSE) can be used in a method for controlling expression of
CC an endoplasmic reticulum chaperone. The method comprises expressing
CC bZIP. The method can be used for expression of a foreign protein by
CC positively regulating expression of an endoplasmic reticulum
CC chaperone gene. bZIP is useful for controlling the expression of
CC endoplasmic reticulum chaperone either positively or negatively in
CC cells and therefore is useful for treatment or prophylaxis of
CC cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases,
CC wounds and ulcers. bZIP also maintains the correct conformation of
CC the endoplasmic reticulum chaperone and thereby increases the
CC expression of a foreign protein. This sequence taken from the
CC glucose regulating protein (GRP) promoter GRP78 contains an ERSE like
CC sequence.
XX SQ Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other;
      Query Match      52.6%; Score 10; DB 21; Length 19;
      Best Local Similarity 52.6%; Pred. No. 1.8e+03;
      Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
Db 1 CCAATCGAGCGCTCCACG 19
      |||||
      |||||

RESULT 14
AAA28573
ID AAA28573 standard; DNA; 19 BP.
AC AAA28573;
XX 29-AUG-2000 (first entry)
DE GRP94 promoter ERSE1-like sequence.
XX Endoplasmic reticulum; stress; ER; transcription factor;
KW transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
KW prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing;
KW cystic fibrosis; ulcer; gene therapy; recombinant gene; human;
KW gene expression; GRP; glucose regulated protein; promoter; ss.
XX Homo sapiens.
OS
XX WO200029429-A2.
PN
XX 25-MAY-2000.
PD
XX 12-NOV-1999; 99WO-JP06305.
PF
XX 13-NOV-1998; 98JP-0324227.
PR
XX 09-JUN-1999; 99JP-0163112.
PX
XX (HSPR-) HSP RES INST INC.
PA
XX Haze K, Yoshida H, Mori K, Yanagi H, Yura T;
PI WPI; 2000-387736/33.
PX
XX New endoplasmic reticulum stress transcription factor (known as bZIP)
PT for controlling expression of endoplasmic reticulum chaperone, useful
PT for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
PT diseases, wounds and ulcers
XX
XX Example 1; Fig 3; 157pp; English.
PS
XX An endoplasmic reticulum stress transcription factor (bZIP)
CC capable of regulating transcription inducing activity exhibited by an
CC element (ERSE) can be used in a method for controlling expression of
CC an endoplasmic reticulum chaperone. The method comprises expressing
CC bZIP. The method can be used for expression of a foreign protein by
CC positively regulating expression of an endoplasmic reticulum
CC chaperone gene. bZIP is useful for controlling the expression of
CC cells and therefore is useful for treatment or prophylaxis of
CC cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases,
CC wounds and ulcers. bZIP also maintains the correct conformation of

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CC positively regulating expression of an endoplasmic reticulum
CC chaperone gene. bZIP is useful for controlling the expression of
CC endoplasmic reticulum chaperone either positively or negatively in
CC cells and therefore is useful for treatment or prophylaxis of
CC cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases,
CC wounds and ulcers. bZIP also maintains the correct conformation of
CC the endoplasmic reticulum chaperone and thereby increases the
CC expression of a foreign protein. This sequence taken from the
CC glucose regulating protein (GRP) promoter GRP94 contains an ERSE like
CC sequence.
XX SQ Sequence 19 BP; 4 A; 10 C; 4 G; 1 T; 0 other;
      Query Match      52.6%; Score 10; DB 21; Length 19;
      Best Local Similarity 52.6%; Pred. No. 1.8e+03;
      Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
Db 1 CCAATCGCGCGCACACG 19
      |||||
      |||||

RESULT 15
AAA28574
ID AAA28574 standard; DNA; 19 BP.
AC AAA28574;
XX 29-AUG-2000 (first entry)
DE GRP94 promoter ERSE1-like sequence.
XX Endoplasmic reticulum; stress; ER; transcription factor;
KW transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
KW prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing;
KW cystic fibrosis; ulcer; gene therapy; recombinant gene; chicken;
KW gene expression; GRP; glucose regulated protein; promoter; ss.
XX Gallus domesticus.
OS
XX WO200029429-A2.
PN
XX 25-MAY-2000.
PD
XX 12-NOV-1999; 99WO-JP06305.
PF
XX 13-NOV-1998; 98JP-0324227.
PR
XX 09-JUN-1999; 99JP-0163112.
PX
XX (HSPR-) HSP RES INST INC.
PA
XX Haze K, Yoshida H, Mori K, Yanagi H, Yura T;
PI WPI; 2000-387736/33.
PX
XX New endoplasmic reticulum stress transcription factor (known as bZIP)
PT for controlling expression of endoplasmic reticulum chaperone, useful
PT for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
PT diseases, wounds and ulcers
XX
XX Example 1; Fig 3; 157pp; English.
PS
XX An endoplasmic reticulum stress transcription factor (bZIP)
CC capable of regulating transcription inducing activity exhibited by an
CC element (ERSE) can be used in a method for controlling expression of
CC an endoplasmic reticulum chaperone. The method comprises expressing
CC bZIP. The method can be used for expression of a foreign protein by
CC positively regulating expression of an endoplasmic reticulum
CC chaperone gene. bZIP is useful for controlling the expression of
CC endoplasmic reticulum chaperone either positively or negatively in
CC cells and therefore is useful for treatment or prophylaxis of
CC cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases,
CC wounds and ulcers. bZIP also maintains the correct conformation of

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CC the endoplasmic reticulum chaperone and thereby increases the  
 CC expression of a foreign protein. This sequence taken from the  
 CC glucose regulating protein (GRP) promoter GRP94 contains an ERSE like  
 CC sequence.  
 XX  
 SQ Sequence 19 BP; 5 A; 7 C; 6 G; 1 T; 0 other;  
 Query Match 52.6%; Score 10; DB 21; Length 19;  
 Best Local Similarity 52.6%; Pred. No. 1.8e+03;  
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 CCAATNNNNNNNNCCACG 19  
 |||||  
 Db 1 CCAATGGGAGCGCACCACG 19  
 |||||

Search completed: December 4, 2003, 08:56:09  
 Job time : 262 secs

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OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 08:47:17 ; Search time 75 Seconds  
(without alignments)  
111.817 Million cell updates/sec

Title: US-09-606-804-1

Perfect score: 19  
Sequence: 1 ccaatnnnnnnnnccacg 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	52.6	19	4	US-09-813-937-1
2	10	52.6	205	4	US-09-313-294A-1696
3	10	52.6	261	4	US-09-389-681-206
4	10	52.6	261	4	US-09-620-405B-206
5	10	52.6	261	4	US-09-339-338-206
6	10	52.6	261	4	US-09-433-826B-206
7	10	52.6	261	4	US-09-604-287A-206
8	10	52.6	270	4	US-09-313-294A-890
9	10	52.6	272	1	US-08-248-474-36
10	10	52.6	282	3	US-08-756-849-36
11	10	52.6	282	4	US-09-252-991A-987
12	10	52.6	285	4	US-09-252-991A-60
13	10	52.6	296	2	US-08-716-942-20
14	10	52.6	296	4	US-09-130-337A-20
15	10	52.6	300	4	US-09-313-294A-7348
16	10	52.6	360	6	5196523-1
17	10	52.6	387	3	US-08-804-372A-23
18	10	52.6	392	4	US-09-404-879A-372
19	10	52.6	399	6	5196523-23
20	10	52.6	421	6	5196523-22
21	10	52.6	424	1	US-08-609-657-15
22	10	52.6	432	4	US-09-252-991A-9959
23	10	52.6	457	4	US-09-702-705-861
24	10	52.6	457	4	US-09-736-457-861
25	10	52.6	467	3	US-09-257-584-8
26	10	52.6	511	4	US-09-702-705-1138
27	10	52.6	511	4	US-09-736-457-1138

C	28	10	52.6	522	4	US-09-663-600A-149	Sequence 149, App
	29	10	52.6	531	4	US-09-222-575-123	Sequence 123, App
	30	10	52.6	531	4	US-09-389-681-123	Sequence 123, App
	31	10	52.6	531	4	US-09-620-405B-123	Sequence 123, App
	32	10	52.6	531	4	US-09-339-338-123	Sequence 123, App
	33	10	52.6	531	4	US-09-433-826B-123	Sequence 123, App
	34	10	52.6	531	4	US-09-604-287A-123	Sequence 123, App
	35	10	52.6	584	4	US-09-663-600A-55	Sequence 55, Appl
	36	10	52.6	641	4	US-09-573-906-7	Sequence 7, Appl
	37	10	52.6	708	4	US-09-252-991A-3364	Sequence 3364, Ap
	38	10	52.6	754	3	US-09-020-956-20	Sequence 20, Appl
	39	10	52.6	754	3	US-09-030-607-20	Sequence 20, Appl
	40	10	52.6	754	4	US-09-439-313-20	Sequence 20, Appl
	41	10	52.6	754	4	US-09-352-616A-20	Sequence 20, Appl
	42	10	52.6	754	4	US-09-232-149A-20	Sequence 20, Appl
	43	10	52.6	770	4	US-09-573-906-6	Sequence 6, Appl
	44	10	52.6	843	4	US-09-171-209-38	Sequence 38, Appl
	45	10	52.6	849	3	US-08-998-416-552	Sequence 552, App

## ALIGNMENTS

## RESULT 1

US-09-813-937-1  
; Sequence 1, Application US/09813937  
; Patent No. 6506600  
; GENERAL INFORMATION:  
; APPLICANT: HERMONAT, Paul L.  
; APPLICANT: MANE, Michael  
; APPLICANT: LIU, Yong  
; TITLE OF INVENTION: SECRETING PRODUCTS FROM SKIN BY ADENO-ASSOCIATED VIRUS (AAV) GEN.  
; TITLE OF INVENTION: TRANSFER  
; FILE REFERENCE: 023533/0116  
; CURRENT APPLICATION NUMBER: US/09/813.937  
; PRIOR FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: US 60/191092  
; PRIOR FILING DATE: 2000-03-22  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: glucose response element  
; NAME/KEY: misc feature  
; LOCATION: (6)-(14)  
; OTHER INFORMATION: "N" at positions 6 - 14 can be A, C, G or T  
US-09-813-937-1

Query Match 52.6%; Score 10; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 1 CCAATNNNNNNNNCCACG 19

## RESULT 2

US-09-313-294A-1696/c  
; Sequence 1696, Application US/09313294A  
; Patent No. 6476212  
; GENERAL INFORMATION:  
; APPLICANT: Lalgudi, Raghunath V.  
; APPLICANT: Ito, Laura Y.  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
; FILE REFERENCE: PL-0017 US  
; CURRENT APPLICATION NUMBER: US/09/313.294A  
; CURRENT FILING DATE: 1999-05-14

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; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 1696
; LENGTH: 205
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700551354H1
US-09-313-294A-1696

Query Match      52.6%; Score 10; DB 4; Length 261;
Best Local Similarity 52.6%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNCCACG 19
Db 122 CCAATCAGACAGACCCACG 104

RESULT 3
US-09-389-681-206
; Sequence 206, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-389-681-206

Query Match      52.6%; Score 10; DB 4; Length 261;
Best Local Similarity 52.6%; Pred. No. 5.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNCCACG 19
Db 140 CCAATTCCTCATCTCCACG 158

RESULT 4
US-09-620-405B-206
; Sequence 206, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-620-405B-206

Query Match      52.6%; Score 10; DB 4; Length 261;
Best Local Similarity 52.6%; Pred. No. 5.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNCCACG 19
Db 140 CCAATTCCTCATCTCCACG 158

RESULT 5
US-09-339-338-206
; Sequence 206, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-339-338-206

Query Match      52.6%; Score 10; DB 4; Length 261;
Best Local Similarity 52.6%; Pred. No. 5.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNCCACG 19
Db 140 CCAATTCCTCATCTCCACG 158

RESULT 6
US-09-433-826B-206
; Sequence 206, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-433-826B-206

Query Match      52.6%; Score 10; DB 4; Length 261;
Best Local Similarity 52.6%; Pred. No. 5.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNCCACG 19
Db 140 CCAATTCCTCATCTCCACG 158
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RESULT 7
US-09-604-287A-206
; Sequence 206, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-206

Query Match          52.6%; Score 10; DB 4; Length 261;
Best Local Similarity 52.6%; Pred. No. 5.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
    |||||
Db 140 CCAATTCCTCATCTCCACG 158

RESULT 8
US-09-313-294A-890/c
; Sequence 890, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 890
; LENGTH: 270
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700550018H1
; NAME/KEY: unsure
; LOCATION: 213-215, 218-221, 232-233, 236-237, 239-240, 242, 249, 251, 253, 261,
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-890

Query Match          52.6%; Score 10; DB 4; Length 270;
Best Local Similarity 52.6%; Pred. No. 5.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
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Db 121 CCAATCAGACAGACCCACG 103

RESULT 9
US-08-248-474-36
; Sequence 36, Application US/08248474
; Patent No. 5612471

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; GENERAL INFORMATION:
; APPLICANT: McK. BIRD, David
; APPLICANT: WILSON, Mark A.
; TITLE OF INVENTION: NEMATODE-INDUCE GENES IN TOMATO
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,474
; FILING DATE: 25-MAY-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 2307E-535
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Lycopersicon esculentum cv 'Rutgers Large
; ORGANISM: Red'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..272
; OTHER INFORMATION: /standard_name= "DB# 155"
US-08-248-474-36

Query Match          52.6%; Score 10; DB 1; Length 272;
Best Local Similarity 52.6%; Pred. No. 5.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
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Db 97 CCAATATTATTACCACG 115

RESULT 10
US-08-756-849-36
; Sequence 36, Application US/08756849
; Patent No. 6093810
; GENERAL INFORMATION:
; APPLICANT: Bird, David McK.
; APPLICANT: Wilson, Mark A.
; TITLE OF INVENTION: Nematode-Induced Genes in Tomato
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/756,849
; FILING DATE: 26-NOV-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,474
; FILING DATE: 25-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-053510US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 base pairs
; TYPE: nucleic acid
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..272
; OTHER INFORMATION: /standard_name="DB# 155"
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; US-08-756-849-36
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Query Match 52.6%; Score 10; DB 3; Length 272;
Best Local Similarity 52.6%; Pred. No. 5.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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```
QY 1 CCAATNNNNNNNNCCACG 19
Db 97 CCAATATTATTTTACCACG 115
```

```
RESULT 11
US-09-252-991A-987
; Sequence 987, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 987
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
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; US-09-252-991A-987
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Query Match 52.6%; Score 10; DB 4; Length 282;
Best Local Similarity 52.6%; Pred. No. 5.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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QY 1 CCAATNNNNNNNNCCACG 19
Db 49 CCAATGCTGATCCCCACG 67
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RESULT 12
US-09-252-991A-60
; Sequence 60, Application US/09252991A
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; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 60
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
;
; US-09-252-991A-60
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Query Match 52.6%; Score 10; DB 4; Length 285;
Best Local Similarity 52.6%; Pred. No. 5.5e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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QY 1 CCAATNNNNNNNNCCACG 19
Db 224 CCAATGACCGATACCACG 242
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## RESULT 13

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US-08-716-942-20/c
; Sequence 20, Application US/08716942
; Patent No. 5849491
; GENERAL INFORMATION:
; APPLICANT: Terragen Diversity Inc.
; APPLICANT: Radomski, Christopher C. A.
; APPLICANT: Seow, Kah Tong
; APPLICANT: Warren, R. Antony J.
; APPLICANT: Yap, Wai Ho
; TITLE OF INVENTION: METHOD FOR ISOLATING XYLANASE GENE
; TITLE OF INVENTION: SEQUENCES FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD AN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,942
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/004,157
; FILING DATE: 20-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: TERR.P-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 296
; TYPE: nucleic acid
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; STRANDEDNESS: DOUBLE
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM:
; FEATURE:
; NAME/KEY: fragment of xylanase gene from degenerate primer
; NAME/KEY: amplification of soil DNA
US-08-716-942-20

Query Match      52.6%; Score 10; DB 2; Length 296;
Best Local Similarity 52.6%; Pred. No. 5.5e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy      1 CCAATNNNNNNNNCCACG 19
Db      217 CCAATGGTTGTGCCACG 199

RESULT 14
US-09-130-337A-20/c
; Sequence 20, Application US/09130337A
; Patent No. 6441148
; GENERAL INFORMATION:
; APPLICANT: Radomski, CCA
; APPLICANT: Seow, KT
; APPLICANT: Warren, RAJ
; APPLICANT: Yap, WH
; TITLE OF INVENTION: METHOD FOR AMPLIFICATION OF XYLANASE GENE FRAGMENTS
; TITLE OF INVENTION: FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD AND COMPOSITIO
; TITLE OF INVENTION: THEREBY
; FILE REFERENCE: 9993-004
; CURRENT APPLICATION NUMBER: US/09/130,337A
; CURRENT FILING DATE: 1998-08-06
; PRIOR APPLICATION NUMBER: 08/716,942
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 60/004,157
; PRIOR FILING DATE: 1995-09-22
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 20
; LENGTH: 296
; TYPE: DNA
; ORGANISM: Unknown organism
; FEATURE:
; OTHER INFORMATION: Description of unknown organism: soil microbe
US-09-130-337A-20

Query Match      52.6%; Score 10; DB 4; Length 296;
Best Local Similarity 52.6%; Pred. No. 5.5e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy      1 CCAATNNNNNNNNCCACG 19
Db      217 CCAATGGTTGTGCCACG 199

RESULT 15
US-09-313-294A-7348/c
; Sequence 7348, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
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; SEQ ID NO 7348
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700381587H1
; NAME/KEY: unsure
; LOCATION: 18, 228, 295
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-7348

Query Match      52.6%; Score 10; DB 4; Length 300;
Best Local Similarity 52.6%; Pred. No. 5.5e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy      1 CCAATNNNNNNNNCCACG 19
Db      292 CCAATCGTACCTCCACG 274

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Job time : 79 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 09:21:30 ; Search time 254 Seconds  
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248.616 Million cell updates/sec

Title: US-09-606-804-1

Perfect score: 19

Sequence: 1 ccaatnnmmnnccacg 19

Scoring table: IDENTITY NUC

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Database : Published Applications NA:

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- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:
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- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:
- 15: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:
- 16: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:
- 17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	10	52.6	24	11	US-09-940-185-207
3	10	52.6	25	9	US-09-402-100-35
4	10	52.6	25	11	US-09-940-185-4188
5	10	52.6	100	10	US-09-969-373-1152
6	10	52.6	123	10	US-09-867-701-3962
7	10	52.6	136	12	US-09-922-449B-18
8	10	52.6	136	12	US-09-922-449B-19
9	10	52.6	142	12	US-09-922-449B-8
10	10	52.6	143	12	US-09-922-449B-24
11	10	52.6	149	12	US-09-922-449B-25
12	10	52.6	150	12	US-09-922-449B-10
13	10	52.6	167	14	US-10-001-883-5
14	10	52.6	210	10	US-09-974-300-8096
15	10	52.6	214	9	US-09-778-320-59
16	10	52.6	214	9	US-09-910-689-59

c	17	10	52.6	214	13	US-10-010-742-59	Sequence 59, Appl
	18	10	52.6	219	10	US-09-783-590-10136	Sequence 10136, A
	19	10	52.6	225	14	US-10-060-036-3284	Sequence 3284, Ap
	20	10	52.6	237	9	US-09-777-564-1013	Sequence 1013, Ap
	21	10	52.6	237	14	US-10-015-219-1013	Sequence 1013, Ap
	22	10	52.6	238	10	US-09-960-352-13155	Sequence 13155, A
	23	10	52.6	247	10	US-09-878-574-6181	Sequence 6181, Ap
	24	10	52.6	261	9	US-09-604-387A-206	Sequence 206, App
	25	10	52.6	261	10	US-09-339-338-206	Sequence 206, App
	26	10	52.6	261	11	US-09-551-621-206	Sequence 206, App
	27	10	52.6	261	12	US-10-124-805-206	Sequence 206, App
	28	10	52.6	261	13	US-10-007-805-206	Sequence 206, App
	29	10	52.6	261	14	US-10-076-622-206	Sequence 206, App
	30	10	52.6	262	12	US-10-099-926-1836	Sequence 1836, Ap
	31	10	52.6	262	13	US-10-033-528-1836	Sequence 1836, Ap
	32	10	52.6	267	9	US-09-294-093B-1896	Sequence 1896, Ap
	33	10	52.6	268	9	US-09-923-876-5857	Sequence 5857, Ap
	34	10	52.6	271	10	US-09-783-590-11139	Sequence 11139, A
	35	10	52.6	272	11	US-09-835-976B-57	Sequence 57, Appl
	36	10	52.6	274	10	US-09-867-701-5278	Sequence 5278, Ap
	37	10	52.6	280	10	US-09-878-574-246	Sequence 246, App
	38	10	52.6	283	9	US-09-294-093B-3259	Sequence 3259, Ap
	39	10	52.6	293	9	US-09-294-093B-6179	Sequence 6179, Ap
	40	10	52.6	301	11	US-09-918-995-24371	Sequence 24371, A
	41	10	52.6	306	10	US-09-974-300-8100	Sequence 8100, Ap
	42	10	52.6	339	10	US-09-878-574-1186	Sequence 1186, Ap
	43	10	52.6	348	11	US-09-899-495-18	Sequence 1451, Ap
	44	10	52.6	351	10	US-09-938-842A-1451	Sequence 1451, Ap
	45	10	52.6	351	10	US-09-796-692-6226	Sequence 6226, Ap

ALIGNMENTS

RESULT 1  
US-10-340-759-1

; Sequence 1, Application US/10340759

; Publication No. US20030104575A1

; GENERAL INFORMATION:

; APPLICANT: HERMONAT, Paul L.

; APPLICANT: MANE, Michael

; APPLICANT: LIU, Yong

; TITLE OF INVENTION: SECRETING PRODUCTS FROM SKIN BY ADENO-ASSOCIATED VIRUS (AAV) GENI

; TITLE OF INVENTION: TRANSFER

; FILE REFERENCE: 023533/0116

; CURRENT APPLICATION NUMBER: US/10/340,759

; CURRENT FILING DATE: 2003-01-13

; PRIOR APPLICATION NUMBER: US/09/813,937A

; PRIOR FILING DATE: 2001-03-22

; PRIOR APPLICATION NUMBER: US 60/191092

; PRIOR FILING DATE: 2000-03-22

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: glucose response element

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (6)..(14)

; OTHER INFORMATION: "N" at positions 6 - 14 can be A, C, G or T

US-10-340-759-1

Query Match 52.6%; Score 10; DB 14; Length 19;

Best Local Similarity 100.0%; Pred No. 4.1e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19

Db 1 CCAATNNNNNNNNCCACG 19

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RESULT 2
US-09-940-185-207/c
; Sequence 207, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 207
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-207

Query Match          52.6%; Score 10; DB 11; Length 24;
Best Local Similarity 52.6%; Pred. No. 4.2e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
    |||||
Db 23 CCAATATTACGTGACCACG 5

RESULT 3
US-09-402-100-35/c
; Sequence 35, Application US/09402100
; Patent No. US20010019834A1
; GENERAL INFORMATION:
; APPLICANT: Daewoong Pharmaceutical Co, LTD
; APPLICANT: Kim, Byung-O
; APPLICANT: Shin, Sung-Seup
; APPLICANT: Yu, Young-Hyo
; APPLICANT: Park, Myung-Hwan
; APPLICANT: Choi, Deok-Joon
; APPLICANT: Jung, Hyung-Jin
; TITLE OF INVENTION: Recombinant Microorganisms Expressing Antigenic Proteins of Helicobacter
; FILE REFERENCE: 0136/OG140
; CURRENT APPLICATION NUMBER: US/09/402,100
; CURRENT FILING DATE: 1999-09-27
; EARLIER APPLICATION NUMBER: KR 97-11950
; EARLIER FILING DATE: 1997-03-31
; EARLIER APPLICATION NUMBER: KR 97-11951
; EARLIER FILING DATE: 1997-03-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..7)
; OTHER INFORMATION: Oligonucleotide
US-09-402-100-35

Query Match          52.6%; Score 10; DB 9; Length 25;
Best Local Similarity 52.6%; Pred. No. 4.2e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
    |||||
Db 23 CCAATATTACGTGACCACG 5

RESULT 4
US-09-940-185-4188/c
; Sequence 4188, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4188
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-4188

Query Match          52.6%; Score 10; DB 11; Length 25;
Best Local Similarity 52.6%; Pred. No. 4.2e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
    |||||
Db 24 CCAATATTACGTGACCACG 6

RESULT 5
US-09-969-373-1152/c
; Sequence 1152, Application US/09969373
; Patent No. US2002013852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 1152
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-1152

Query Match          52.6%; Score 10; DB 10; Length 100;
Best Local Similarity 52.6%; Pred. No. 4.9e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
    |||||
Db 97 CCAATCATTTCATCCACG 79

RESULT 6
US-09-867-701-3962
; Sequence 3962, Application US/09867701
```

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Db 20 CCAATTTTACCATCCACG 2

RESULT 4
US-09-940-185-4188/c
; Sequence 4188, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4188
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-4188

Query Match          52.6%; Score 10; DB 11; Length 25;
Best Local Similarity 52.6%; Pred. No. 4.2e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
    |||||
Db 24 CCAATATTACGTGACCACG 6

RESULT 5
US-09-969-373-1152/c
; Sequence 1152, Application US/09969373
; Patent No. US2002013852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 1152
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-1152

Query Match          52.6%; Score 10; DB 10; Length 100;
Best Local Similarity 52.6%; Pred. No. 4.9e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
    |||||
Db 97 CCAATCATTTCATCCACG 79

RESULT 6
US-09-867-701-3962
; Sequence 3962, Application US/09867701
```

; Patent No. US2002013237A1  
; GENERAL INFORMATION:  
; APPLICANT: Aglate, Paul A.  
; APPLICANT: Jones, Robert  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.497  
; CURRENT APPLICATION NUMBER: US/09/867,701  
; CURRENT FILING DATE: 2001-05-29  
; NUMBER OF SEQ ID NOS: 10912  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3962  
; LENGTH: 123  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-867-701-3962

Query Match 52.6%; Score 10; DB 10; Length 123;  
Best Local Similarity 52.6%; Pred. No. 5e+03;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNCCACG 19  
|||||  
Db 4 CCAATCTGTCGGACCACG 22

## RESULT 7

US-09-922-449B-18  
; Sequence 18, Application US/09922449B  
; Publication No. US20030148278A1  
; GENERAL INFORMATION:  
; APPLICANT: BioInside Gesellschaft fur Biodiagnostik, Auftragsforschung und Consulting  
; APPLICANT: mbH  
; TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically modified  
; TITLE OF INVENTION: in foodstuff by means of fluorescent-coupled PCR  
; FILE REFERENCE: 101215-68  
; CURRENT APPLICATION NUMBER: US/09/922,449B  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: PCT/EP00/009835  
; PRIOR FILING DATE: 2000-02-07  
; PRIOR APPLICATION NUMBER: DE 199 06 169.6  
; PRIOR FILING DATE: 1999-02-08  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 18  
; LENGTH: 136  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: target IAC DNA for the Bt-176  
US-09-922-449B-18

Query Match 52.6%; Score 10; DB 12; Length 136;  
Best Local Similarity 52.6%; Pred. No. 5.1e+03;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNCCACG 19  
|||||  
Db 27 CCAATTTTCGCTCCACG 45

## RESULT 8

US-09-922-449B-19  
; Sequence 19, Application US/09922449B  
; Publication No. US20030148278A1  
; GENERAL INFORMATION:  
; APPLICANT: BioInside Gesellschaft fur Biodiagnostik, Auftragsforschung und Consulting  
; APPLICANT: mbH  
; TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically modified  
; TITLE OF INVENTION: in foodstuff by means of fluorescent-coupled PCR  
; FILE REFERENCE: 101215-68

; CURRENT APPLICATION NUMBER: US/09/922,449B  
; CURRENT FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: PCT/EP00/009835  
; PRIOR FILING DATE: 2000-02-07  
; PRIOR APPLICATION NUMBER: DE 199 06 169.6  
; PRIOR FILING DATE: 1999-02-08  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 19  
; LENGTH: 136  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: reference IAC DNA for the Bt-176  
US-09-922-449B-19

Query Match 52.6%; Score 10; DB 12; Length 136;  
Best Local Similarity 52.6%; Pred. No. 5.1e+03;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNCCACG 19  
|||||  
Db 27 CCAATTTTCGCTCCACG 45

## RESULT 9

US-09-922-449B-8  
; Sequence 8, Application US/09922449B  
; Publication No. US20030148278A1  
; GENERAL INFORMATION:  
; APPLICANT: BioInside Gesellschaft fur Biodiagnostik, Auftragsforschung und Consulting  
; APPLICANT: mbH  
; TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically modified  
; TITLE OF INVENTION: in foodstuff by means of fluorescent-coupled PCR  
; FILE REFERENCE: 101215-68  
; CURRENT APPLICATION NUMBER: US/09/922,449B  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: PCT/EP00/009835  
; PRIOR FILING DATE: 2000-02-07  
; PRIOR APPLICATION NUMBER: DE 199 06 169.6  
; PRIOR FILING DATE: 1999-02-08  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 142  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: target IAC DNA for the RRS 9e  
US-09-922-449B-8

Query Match 52.6%; Score 10; DB 12; Length 142;  
Best Local Similarity 52.6%; Pred. No. 5.1e+03;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNCCACG 19  
|||||  
Db 31 CCAATTTTCGCTCCACG 49

## RESULT 10

US-09-922-449B-24  
; Sequence 24, Application US/09922449B  
; Publication No. US20030148278A1  
; GENERAL INFORMATION:  
; APPLICANT: BioInside Gesellschaft fur Biodiagnostik, Auftragsforschung und Consulting  
; APPLICANT: mbH  
; TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically modified  
; TITLE OF INVENTION: in foodstuff by means of fluorescent-coupled PCR  
; FILE REFERENCE: 101215-68  
; CURRENT APPLICATION NUMBER: US/09/922,449B  
; CURRENT FILING DATE: 2001-08-03

; PRIOR APPLICATION NUMBER: PCT/EP00/009835  
; PRIOR FILING DATE: 2000-02-07  
; PRIOR APPLICATION NUMBER: DE 199 06 169.6  
; PRIOR FILING DATE: 1999-02-08  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 24  
; LENGTH: 143  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: target IAC DNA for the RRS ge  
US-09-922-449B-24

Query Match 52.6%; Score 10; DB 12; Length 143;

Best Local Similarity 52.6%; Pred. No. 5.1e+03;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19  
|||||  
Db 31 CCAATTTTCGCTCCACG 49

## RESULT 11

US-09-922-449B-25  
; Sequence 25, Application US/09922449B  
; Publication No. US20030148278A1  
; GENERAL INFORMATION:  
; APPLICANT: BioInside Gesellschaft fur Bodiagnostik, Auftragsforschung und Consulting  
; APPLICANT: mbH  
; TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically modified  
; FILE OF INVENTION: in foodstuff by means of fluorescent-coupled PCR  
; FILE REFERENCE: 101215-68  
; CURRENT APPLICATION NUMBER: US/09/922,449B  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: PCT/EP00/009835  
; PRIOR FILING DATE: 2000-02-07  
; PRIOR APPLICATION NUMBER: DE 199 06 169.6  
; PRIOR FILING DATE: 1999-02-08  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 25  
; LENGTH: 149  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: reference IAC DNA for the RRS  
US-09-922-449B-25

Query Match 52.6%; Score 10; DB 12; Length 149;

Best Local Similarity 52.6%; Pred. No. 5.1e+03;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19  
|||||  
Db 31 CCAATTTTCGCTCCACG 49

## RESULT 12

US-09-922-449B-10  
; Sequence 10, Application US/09922449B  
; Publication No. US20030148278A1  
; GENERAL INFORMATION:  
; APPLICANT: BioInside Gesellschaft fur Bodiagnostik, Auftragsforschung und Consulting  
; APPLICANT: mbH  
; TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically modified  
; FILE OF INVENTION: in foodstuff by means of fluorescent-coupled PCR  
; FILE REFERENCE: 101215-68  
; CURRENT APPLICATION NUMBER: US/09/922,449B  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: PCT/EP00/009835  
; PRIOR FILING DATE: 2000-02-07

; PRIOR APPLICATION NUMBER: DE 199 06 169.6  
; PRIOR FILING DATE: 1999-02-08  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 150  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: reference IAC DNA for the RRS  
US-09-922-449B-10

Query Match 52.6%; Score 10; DB 12; Length 150;

Best Local Similarity 52.6%; Pred. No. 5.1e+03;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19  
|||||  
Db 32 CCAATTTTCGCTCCACG 50

## RESULT 13

US-10-001-883-5/c  
; Sequence 5, Application US/10001883  
; Publication No. US20030022188A1  
; GENERAL INFORMATION:  
; APPLICANT: Macina, Roberto  
; APPLICANT: Recipon, Herve  
; APPLICANT: Pluta, Jason  
; APPLICANT: Ghosh, Malavika  
; APPLICANT: Sun, Yongming  
; APPLICANT: Liu, Chenghua  
; TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Pro  
; FILE REFERENCE: DEX-0271  
; CURRENT APPLICATION NUMBER: US/10/001,883  
; PRIOR FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/252,059  
; PRIOR FILING DATE: 2000-11-20  
; NUMBER OF SEQ ID NOS: 137  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 167  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-001-883-5

Query Match 52.6%; Score 10; DB 14; Length 167;

Best Local Similarity 52.6%; Pred. No. 5.2e+03;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19  
|||||  
Db 160 CCAATTTTGGAAATCACCACG 142

## RESULT 14

US-09-974-300-8096/c  
; Sequence 8096, Application US/09974300  
; Patent No. US20020146721A1  
; GENERAL INFORMATION:  
; APPLICANT: Berka, Randy M.  
; APPLICANT: Clausen, Ib Groth  
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
; FILE OF INVENTION: Expression  
; FILE REFERENCE: 10085.500-US  
; CURRENT APPLICATION NUMBER: US/09/974,300  
; PRIOR FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: 09/680,598  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/279,526  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 8481

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8096
; LENGTH: 210
; TYPE: DNA
; ORGANISM: Bacillus clausii
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(210)
; OTHER INFORMATION: n = A,T,C or G
US-09-974-300-8096
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Query Match          52.6%; Score 10; DB 10; Length 210;
Best Local Similarity 52.6%; Pred. No. 5.3e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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```
Qy      1 CCAATNNNNNNCCACG 19
        |||||
Db      152 CCAATTCGTCGTCCACG 134
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## RESULT 15

```
US-09-778-320-59/c
; Sequence 59, Application US/09778320
; Patent No. US20010034052A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongrong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491CS
; CURRENT APPLICATION NUMBER: US/09/778,320
; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 214
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(214)
; OTHER INFORMATION: n = A,T,C or G
US-09-778-320-59
```

```
Query Match          52.6%; Score 10; DB 9; Length 214;
Best Local Similarity 52.6%; Pred. No. 5.3e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
```

```
Qy      1 CCAATNNNNNNCCACG 19
        |||||
Db      88 CCAATTCGTCGTCCACG 70
```

Search completed: December 4, 2003, 10:57:37  
Job time : 257 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 05:58:56 ; Search time 2068 Seconds  
(without alignments)  
223.300 Million cell updates/sec

Title: US-09-606-804-1

Perfect score: 19

Sequence: 1 ccaatnnnnnnnnccacg 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hcc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hcc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	52.6	43	28	BH857113
C 2	10	52.6	47	29	BX292617
C 3	10	52.6	58	29	AL949322
4	10	52.6	76	9	AA475936

5	10	52.6	79	13	B0756881
C 6	10	52.6	80	9	AL897168
C 7	10	52.6	80	28	BH251489
8	10	52.6	82	13	BQ099298
C 9	10	52.6	86	28	BH232183
C 10	10	52.6	97	28	BH222106
C 11	10	52.6	99	14	CB338675
C 12	10	52.6	99	28	AZ921866
C 13	10	52.6	100	10	BF086094
14	10	52.6	101	28	BH583741
C 15	10	52.6	103	9	AA927925
C 16	10	52.6	109	28	BH864991
17	10	52.6	110	10	BF094257
18	10	52.6	110	28	AZ720239
19	10	52.6	112	29	BZ662888
C 20	10	52.6	113	28	BH222899
21	10	52.6	114	29	CC458196
22	10	52.6	115	9	A1938545
23	10	52.6	115	10	AW945325
C 24	10	52.6	115	12	BG950375
25	10	52.6	115	13	BW091136
26	10	52.6	115	29	CC029017
27	10	52.6	115	29	AG024826
28	10	52.6	116	29	CC037007
C 29	10	52.6	119	9	A1549504
C 30	10	52.6	120	28	BH230343
31	10	52.6	120	28	BH905244
C 32	10	52.6	121	14	CB097190
C 33	10	52.6	121	28	BH222096
34	10	52.6	123	9	AA405167
35	10	52.6	124	28	AQ073902
C 36	10	52.6	124	28	BH812753
C 37	10	52.6	124	28	BH847929
C 38	10	52.6	129	28	AZ919927
39	10	52.6	130	28	BH895687
40	10	52.6	130	29	BZ663067
41	10	52.6	131	29	BZ386507
42	10	52.6	132	10	BF361951
43	10	52.6	132	10	BE936064
44	10	52.6	132	28	BH753521
45	10	52.6	132	28	BH854781

## ALIGNMENTS

RESULT 1  
BH857113  
LOCUS

DEFINITION

BH857113 43 bp DNA linear GSS 08-JUL-2002  
SALK\_076821.44.95.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_076821.44.95.x, genomic  
survey sequence.

ACCSSION

VERSION BH857113.1 GI:21707434

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

1 (bases 1 to 43)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab

,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.

, Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu  
 This is single pass sequence recovered from the left border of  
 TDNA. This sequence lies within an annotated exon of At4g29100.  
 Class: TDNA tagged.

#### FEATURES

Location/Qualifiers

1..43  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_076821.44.95.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"  
 BASE COUNT 11 a 11 c 10 g 11 t  
 ORIGIN

Query Match 52.6%; Score 10; DB 28; Length 43;  
 Best Local Similarity 52.6%; Pred. No. 2e+04;  
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19  
 ||||| |||||  
 Db 18 CCAATGAATACGCCACG 36

#### RESULT 2

BX292617/c  
 LOCUS 47 bp DNA linear GSS 07-MAR-2003  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-455E08-018778,  
 genomic survey sequence.

ACCESSION BX292617  
 VERSION BX292617.1 GI:28891613  
 KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.  
 and Weisshaar,B.  
 A pipeline for automated high-throughput generation of FSTs  
 (flanking sequence tags) from Arabidopsis thaliana T-DNA  
 transformed lines

JOURNAL Unpublished  
 REFERENCE 2 Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.  
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
 for flanking sequence tag based reverse genetics

AUTHORS Unpublished  
 TITLE Unpublished

JOURNAL 3 (bases 1 to 47)

AUTHORS Li,Y., Strizhov,N., Rosso,M. and Weisshaar,B.

TITLE Direct Submission

JOURNAL Submitted (07-MAR-2003) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence is recovered from the left border of the T-DNA. It

indicates an insertion within the locus defined by clone f1913. The

sequences are generated at the MPI for Plant Breeding Research in

the context of the GABI-Kat project. GABI-Kat is part of the German

Plant Genomics program designated 'GABI'. Information on line

availability can be found at:

<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

Location/Qualifiers

1..47

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

#### FEATURES

source

/clone="CK-455E08-018778"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /note="PCR was performed on DNA from Arabidopsis thaliana  
 plants (T1) which were transformed with the T-DNA from  
 vector pAC161. The lines contain one or more T-DNA  
 insertions. The DNA fragment(s) resulting from the PCR  
 were directly sequenced to determine the genomic sequence  
 flanking the insertion. Sequences displaying significant  
 similarity to the A. thaliana nuclear genome sequences were  
 processed for submission. T-DNA derived sequences were  
 removed"  
 BASE COUNT 17 a 4 c 10 g 16 t  
 ORIGIN

Query Match 52.6%; Score 10; DB 29; Length 47;  
 Best Local Similarity 52.6%; Pred. No. 2.1e+04;  
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19  
 ||||| |||||  
 Db 22 CCAATAAAACTCTCCACG 4

#### RESULT 3

AL949322/c

LOCUS 58 bp DNA linear GSS 24-OCT-2002

DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-319H03-015860,  
 genomic survey sequence.

ACCESSION AL949322

VERSION AL949322.1 GI:24405944

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.  
 and Weisshaar,B.  
 A pipeline for automated high-throughput generation of FSTs  
 (flanking sequence tags) from Arabidopsis thaliana T-DNA  
 transformed lines

JOURNAL Unpublished

REFERENCE 2 Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.  
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
 for flanking sequence tag based reverse genetics

AUTHORS Unpublished

TITLE Unpublished

JOURNAL 3 (bases 1 to 58)

AUTHORS Rosso,M., Strizhov,N., Li,Y. and Weisshaar,B.

TITLE Direct Submission

JOURNAL Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence is recovered from the left border of the T-DNA. It

indicates an insertion close to or within gene Atlg50730. The

sequences are generated at the MPI for Plant Breeding Research in

the context of the GABI-Kat project. GABI-Kat is part of the German

Plant Genomics program designated 'GABI'. Information on line

availability can be found at:

<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

Location/Qualifiers

1..58

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="GK-319H03-015860"

/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"

/note="PCR was performed on DNA from Arabidopsis thaliana  
 plants (T1) which were transformed with the T-DNA from  
 vector pAC161. The lines contain one or more T-DNA  
 insertions. The DNA fragment(s) resulting from the PCR  
 were directly sequenced to determine the genomic sequence

removed"

BASE COUNT 17 a 4 c 10 g 16 t

ORIGIN

flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

```

BASE COUNT      21 a  11 c  10 g  16 t
ORIGIN
Query Match      52.6%; Score 10; DB 29; Length 58;
Best Local Similarity 52.6%; Pred. No. 2.3e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
    |||||
Db 34 CCAATCTGTGTAGCCACG 16
    |||||

```

```

RESULT 4
AA475936
LOCUS
DEFINITION
Vn25b10.t1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone
IMAGE:876475 5' similar to TR:E196749 E196749 MRNA; EXPRESSED
SEQUENCE TAG ;, MRNA sequence.

```

```

ACCESSION
AA475936
VERSION
AA475936.1 GI:2203787
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

```

```

REFERENCE
AUTHORS
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

```

```

TITLE
The WashU-HMI Mouse EST Project
JOURNAL
Unpublished
COMMENT
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu

```

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:515955

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28m13 rev2 ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

FEATURES

source

```

1. .76
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:876475"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares_mammary_gland_NbMMG"
/notes="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
) with a modified polylinker; Site.1: Not I; Site.2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5',
TGTTACCAATCTGAATGGAGCGCGCCGAAATGGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima

```

```

BASE COUNT      19 a  28 c  16 g  13 t
ORIGIN
Query Match      52.6%; Score 10; DB 9; Length 76;
Best Local Similarity 52.6%; Pred. No. 2.5e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

```

Qy 1 CCAATNNNNNNNNCCACG 19
    |||||
Db 40 CCAATGGTTTAGCCACG 58
    |||||

```

```

RESULT 5
BQ756881
LOCUS
DEFINITION
EBem09_SQ005_E15_R embryo, 1 Day germination, no treatment, cv
Optic, EBem09_Hordeum vulgare subsp. vulgare cDNA clone
EBem09_SQ005_E15 5', mRNA sequence.

```

```

ACCESSION
BQ756881
VERSION
BQ756881.1 GI:21965353
KEYWORDS
EST.
SOURCE
Hordeum vulgare subsp. vulgare
ORGANISM
Hordeum vulgare subsp. vulgare

```

```

REFERENCE
AUTHORS
Hadley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardie,L.,
Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
Development of Barley Transcriptome Resources
Unpublished
Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk.

```

```

TITLE
Development of Barley Transcriptome Resources
JOURNAL
Unpublished
COMMENT
Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk.

```

```

FEATURES
source
1. .79
Location/Qualifiers
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Optic"
/db_xref="taxon:112509"
/clone="EBem09_SQ005_E15"
/tissue_type="embryo"
/dev_stage="1 Day germination"
/lab_host="DH10B"
/clone_lib="embryo, 1 Day germination, no treatment, cv
Optic, EBem09"
/notes="Vector: pSPORT1; Site.1: Sal I; Site.2: Not I;
Non-normalised library, directionally cloned into pSPORT1.
Derived from embryos dissected from germinating grains (1
day) in glasshouse grown barley plants. Developed as part
of the barley transcriptome resources of BBSRC/SEERAD
funded cereal 1Gf (Investigating Gene Function) project."

```

```

BASE COUNT      19 a  18 c  17 g  25 t
ORIGIN
Query Match      52.6%; Score 10; DB 13; Length 79;
Best Local Similarity 52.6%; Pred. No. 2.6e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

```

Qy 1 CCAATNNNNNNNNCCACG 19
    |||||
Db 42 CCAATTTTGTCAACACG 60
    |||||

```

```

RESULT 6
AL897168/c
LOCUS
DEFINITION
AL897168 XGC-egg Silurana tropicalis cDNA clone TEGg01ld06 3', mRNA

```

```

BASE COUNT      19 a  18 c  17 g  25 t
ORIGIN
Query Match      52.6%; Score 10; DB 13; Length 79;
Best Local Similarity 52.6%; Pred. No. 2.6e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

```

Qy 1 CCAATNNNNNNNNCCACG 19
    |||||
Db 42 CCAATTTTGTCAACACG 60
    |||||

```

```

RESULT 6
AL897168/c
LOCUS
DEFINITION
AL897168 XGC-egg Silurana tropicalis cDNA clone TEGg01ld06 3', mRNA

```



revealed the presence of an additional Trichostrongyloidea cattle nematode, *Cooperia oncophora*. Sequences in this library may derive from either *Ostertagia* or *Cooperia*. The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMPI. Nematodes were provided by Dr. Louis Gasbarre of the USDA, Beltsville, MD (lgasbarre@nri.barc.usda.gov). Third stage exsheathed larvae were collected from 14 day fecal-sphagnum moss cultures of *Ostertagia* eggs. The larvae were recovered by overnight passage on a Baermann apparatus, and then cleaned by passage through a 20 micron nylon mesh. The larvae were then subjected to a treatment with 1.25% chlorox to induce excystation. The larvae were washed with 5 changes of PBS and then pelleted and snap frozen in liquid nitrogen."

BASE COUNT 24 a 24 c 12 g 22 t  
ORIGIN

Query Match 52.6%; Score 10; DB 13; Length 82;  
Best Local Similarity 52.6%; Pred. No. 2.6e+04;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19  
|||||  
Db 12 CCAATGGAGAGTGTCACG 30

RESULT 9  
BH232183/c  
LOCUS  
DEFINITION BH232183 86 bp DNA linear GSS 08-NOV-2001  
1006166D12.V1 1006 - RescueMu Grid G Zea mays genomic, genomic survey sequence.

ACCESSION  
VERSION BH232183.1 GI:16837119  
KEYWORDS  
SOURCE GSS.  
ORGANISM Zea mays

REFERENCE  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
TITLE 1 (bases 1 to 86)  
JOURNAL Walbot, V.

COMMENT  
Maize genomic sequences found using engineered RescueMu transposon  
Unpublished  
Contact: Walbot V

Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Possible ligation site so sequence was trimmed. Post-ligation sequence submitted separately.  
Plate: 1006166 row: 23  
Class: transposon-tagged.  
Location/Qualifiers

FEATURES  
source  
1..86  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1006 - RescueMu Grid G"  
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA."

Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu'. Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 13 a 24 c 37 g 12 t  
ORIGIN

Query Match 52.6%; Score 10; DB 28; Length 86;  
Best Local Similarity 52.6%; Pred. No. 2.6e+04;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19  
|||||  
Db 61 CCAATCATTTGGACGCCACG 43

RESULT 10  
BH222106/c  
LOCUS  
DEFINITION BH222106 97 bp DNA linear GSS 08-NOV-2001  
1006105C10.X1 1006 - RescueMu Grid G Zea mays genomic, genomic survey sequence.

ACCESSION  
VERSION BH222106.1 GI:16816606  
KEYWORDS  
SOURCE GSS.  
ORGANISM Zea mays

REFERENCE  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
TITLE 1 (bases 1 to 97)  
JOURNAL Walbot, V.

COMMENT  
Maize genomic sequences found using engineered RescueMu transposon  
Unpublished  
Contact: Walbot V

Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 1006105 row: 13  
Class: transposon-tagged.  
Location/Qualifiers

FEATURES  
source  
1..97

/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1006 - RescueMu Grid G"  
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA."  
Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu'. Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 11 a 27 c 44 g 15 t  
ORIGIN

Query Match 52.6%; Score 10; DB 28; Length 97;  
Best Local Similarity 52.6%; Pred. No. 2.8e+04;

```

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNCCACG 19
    |||||
Db 92 CCAATTGAGCACCACG 74

RESULT 11
CB338675/c
LOCUS
DEFINITION
  CB338675 99 bp mRNA linear EST 13-MAR-2003
  kb5904.y1 Brugia malayi L3 pAMP1 v2 Brugia malayi cDNA 5' similar
  to TOR16159 O16159 CYSTATIN-TYPE CYSTEINE PROTEINASE INHIBITOR. ;,
  mRNA sequence.
ACCESSION
  CB338675
VERSION
  CB338675.1 GI:28941376
KEYWORDS
  EST.
SOURCE
  Brugia malayi
  Brugia malayi
  Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
  Onchocercidae; Brugia.
REFERENCE
  1 (bases 1 to 99)
AUTHORS
  McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.,
  Dante,M., Maria,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,
  Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Teagareishvili,R.,
  Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
  M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
  Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
  Wilson,R.
  The Washington Univ. Nematode EST Project, 1999
  Unpublished
  Contact: McCarter JP
  The Washington Univ. Nematode EST Project, 1999
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  Nematodes were provided by Dr. Ben-Wen Li and Dr. Gary Weil of
  Washington University, St. Louis, MO (weillab@ingate.wustl.edu).
  Seq primer: -4ORP from Gibco.
FEATURES
  source
  1..99
  /organism="Brugia malayi"
  /mol_type="mRNA"
  /db_xref="taxon:6279"
  /dev_stage="L3"
  /lab_host="DH10B"
  /clone_lib="Brugia malayi L3 pAMP1 v2"
  /notes="Vector: pAMP1(Invitrogen); Site_1: NotI; Site_2:
  SalI; The library was constructed by Amy Rush, Claire
  Murphy and Dr. James McCarter at Washington University,
  St. Louis. The cDNA was made by using Dynabead oligo-dT
  priming (Dynal). PCR based library using a modified
  protocol from the SMART PCR cDNA Synthesis Kit from
  Clontech. Directionally cloned into the UDG sites of
  pAMP1. Nematodes were provided by Dr. Ben-Wen Li and Dr.
  Gary Weil of Washington University, St. Louis, MO
  (weillab@ingate.wustl.edu)."
```

BASE COUNT 31 a 16 c 21 g 31 t

Query Match 52.6%; Score 10; DB 14; Length 99;  
 Best Local Similarity 52.6%; Pred. No. 2.8e+04;  
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNCCACG 19  
 |||||

Db

RESULT 12

AZ921866/c

LOCUS

AZ921866

99 bp DNA

linear

GSS 07-JUN-2002

DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

HRCot4D10 Sorghum bicolor HRCot Sorghum bicolor genomic, genomic  
 survey sequence.  
 AZ921866  
 AZ921866.1 GI:13400225  
 GSS.  
 Sorghum bicolor (sorghum)

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Plant Genome Mapping Laboratory  
 University of Georgia  
 Room 162, Riverbend Research Bldg., 110 Riverbend Rd., Athens, GA  
 30602, USA  
 Tel: 706-583-0167  
 Fax: 706-583-0160  
 Email: dgpearches.uga.edu  
 Class: Hydroxyapatite-fractionated DNA.

Location/Qualifiers

1..99

/organism="Sorghum bicolor"

/mol\_type="genomic DNA"

/cultivar="BTx623"

/db\_xref="taxon:4558"

/tissue\_type="leaves"

/dev\_stage="seedling"

/clone\_lib="Sorghum bicolor HRCot"

/notes="Vector: pGEM-TA-Easy; A Cot analysis was performed  
 for the sorghum genome. Based on the resulting Cot curve,  
 hydroxyapatite chromatography was used to isolate  
 'highly-repetitive' (HR), 'moderately-repetitive' (MR),  
 and 'single/low-copy' (SL) sequence components from  
 sheared genomic DNA. The three repetition-based DNA  
 components were cloned into E. coli to produce HRCot,  
 MRCot, and SLCot genomic libraries. Blotting and  
 sequencing data indicates that each library is  
 representative of the component from which it was derived.  
 Putative ID listings given for sequences are based on  
 comparison (blastn) with sequences in the NCBI Nr  
 Database. Only the primary match is given (all primary E  
 values are < or = 1.00E-5). In no instance does a 'Cot  
 clone' contain the complete sequence of its putative Nr  
 match."

BASE COUNT 18 a 19 c 29 g 33 t

ORIGIN

Query Match 52.6%; Score 10; DB 28; Length 99;  
 Best Local Similarity 52.6%; Pred. No. 2.8e+04;  
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNCCACG 19  
 |||||

Db 56 CCAATTGCAATCTCCACG 38  
 |||||

RESULT 13

BF086094

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BF086094  
 CM3-GN0052-080900-334-cl1 GN0052 Homo sapiens cDNA, mRNA sequence.  
 BF086094  
 BF086094.1 GI:10891804  
 EST.  
 Homo sapiens (human)  
 Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

#### REFERENCE AUTHORS

1 (bases 1 to 100)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

#### TITLE

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

#### JOURNAL MEDLINE

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

#### PUBMED COMMENT

20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=CM3-GN0052-080>)  
900-334-clit&t3=2000-09-08&t4=1  
Seq primer: puc 18 forward  
High quality sequence start: 5  
High quality sequence stop: 100.

#### FEATURES source

1..100  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="adult"  
/clone\_lib="GN0052"  
/notes="Organ: placenta normal; Vector: puc18; Site 1: SmaI ; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
35 a 23 c 18 g 24 t

#### BASE COUNT ORIGIN

Query Match 52.6%; Score 10; DB 10; Length 100;  
Best Local Similarity 52.6%; Pred. No. 2.8e+04;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19

|||||  
Db 82 CCAATTCGAATCCACG 100

#### RESULT 14 BH583741

LOCUS BH583741 101 bp DNA linear GSS 15-DEC-2001  
BOGXN16TR BOGX Brassica oleracea genomic clone BOGXN16, genomic survey sequence.

#### ACCESSION VERSION

BH583741

#### KEYWORDS SOURCE

BH583741.1 GI:17836198

#### ORGANISM

Brassica oleracea  
Brassica oleracea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids II; Brassicales; Brassicaceae; Brassica.

#### REFERENCE

1 (bases 1 to 101)  
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.  
Whole genome shotgun sequencing of Brassica oleracea  
Unpublished  
Contact: Chris Town

#### JOURNAL COMMENT

Unpublished

#### TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
DNA is from a doubled haploid provided by Tom Osborn.  
Seq primer: TR  
Class: sheared ends.

#### FEATURES source

Location/Qualifiers  
1..101  
/organism="Brassica oleracea"  
/mol\_type="genomic DNA"  
/strain="T01000DH3"  
/db\_xref="taxon:3712"  
/clone="BOGXN16"  
/clone\_lib="BOGX"  
/notes="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"  
38 a 23 c 22 g 18 t

#### BASE COUNT ORIGIN

Query Match 52.6%; Score 10; DB 28; Length 101;  
Best Local Similarity 52.6%; Pred. No. 2.8e+04;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19

|||||  
Db 25 CCAATCGGGCGCCGCCACG 43

#### RESULT 15 AA927925/c

LOCUS AA927925/c 103 bp mRNA linear EST 10-JUN-1998  
DEFINITION Om23b01.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1541833 3', mRNA sequence.

#### ACCESSION VERSION

AA927925

#### KEYWORDS SOURCE

AA927925.1 GI:3076669

#### ORGANISM

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

#### REFERENCE

1 (bases 1 to 103)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

#### JOURNAL COMMENT

Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapsb@mail.nih.gov  
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Insert Length: 553 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 57.

#### FEATURES source

Location/Qualifiers  
1..103  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1541833"  
/lab\_host="DH10B"  
/clone\_lib="Soares\_NFL\_T\_GBC\_S1"  
/notes="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI CGAP GCBI) were mixed and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento

Soares and M. Fatima Bonaldo. "

BASE COUNT  
ORIGIN

25 a 23 c 25 g 30 t

Query Match 52.6%; Score 10; DB 9; Length 103;

Best Local Similarity 52.6%; Pred. No. 2.8e+04;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNCCACG 19

Db 55 CCAATTCAATCGGACCACG 37

Search completed: December 4, 2003, 07:47:50  
Job time : 2077 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 08:43:06 ; Search time 2143 Seconds  
(without alignments)  
215.485 Million cell updates/sec

Title: US-09-606-804-1

Perfect score: 19

Sequence: 1 ccaatnnnnnnnccacg 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmuv:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	52.6	43	28	BH857113
C 2	10	52.6	47	29	BX292617
C 3	10	52.6	58	29	AL949322
4	10	52.6	76	9	AA475936

5	10	52.6	79	13	BQ756881
C 6	10	52.6	80	9	AL897168
C 7	10	52.6	80	28	BH251489
8	10	52.6	82	13	BQ099298
C 9	10	52.6	86	28	BH232183
C 10	10	52.6	97	28	BH222106
C 11	10	52.6	99	14	CB338675
C 12	10	52.6	99	28	AZ921866
C 13	10	52.6	100	10	BF086094
14	10	52.6	101	28	BH583741
C 15	10	52.6	103	9	AA927925
C 16	10	52.6	109	28	BH864991
17	10	52.6	110	10	BF094257
18	10	52.6	110	28	AZ720239
19	10	52.6	112	29	BZ662888
C 20	10	52.6	113	28	BH222899
21	10	52.6	114	29	CC458196
22	10	52.6	115	9	AI938545
23	10	52.6	115	10	AW945325
C 24	10	52.6	115	12	BG950375
25	10	52.6	115	13	BW091136
26	10	52.6	115	29	CC029017
27	10	52.6	115	29	AG024826
28	10	52.6	116	29	CC037007
C 29	10	52.6	119	9	AI549504
C 30	10	52.6	120	28	BH230343
C 31	10	52.6	120	28	BH905244
C 32	10	52.6	121	14	CB097190
C 33	10	52.6	121	28	BH222096
34	10	52.6	123	9	AA405167
35	10	52.6	124	28	AQ073902
C 36	10	52.6	124	28	BH812753
C 37	10	52.6	124	28	BH847929
C 38	10	52.6	129	28	AZ919927
39	10	52.6	130	28	BH895687
40	10	52.6	130	29	BZ663067
41	10	52.6	131	29	BZ386507
42	10	52.6	132	10	BF361951
43	10	52.6	132	10	BE936084
44	10	52.6	132	28	BH753521
45	10	52.6	132	28	BH854781

## ALIGNMENTS

RESULT 1  
BH857113  
LOCUS

DEFINITION

BH857113 43 bp DNA linear GSS 08-JUL-2002  
SALK\_076821.44.95.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_076821.44.95.x, genomic  
survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379



flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

BASE COUNT 21 a 11 c 10 g 16 t

ORIGIN

Query Match 52.6%; Score 10; DB 29; Length 58;  
Best Local Similarity 52.6%; Pred. No. 2.3e+04;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19  
|||||

Db 34 CCAATCTGTGTAGCCACG 16  
|||||

RESULT 4  
LOCUS AA475936 76 bp mRNA linear EST 18-JUN-1997  
DEFINITION VM5B10.r1 Soares mammary\_gland NbMMG Mus musculus cDNA clone  
IMAGE:876475 5' similar to TR:E196749 E196749 MRNA; EXPRESSED  
SEQUENCE TAG ;, mRNA sequence.

ACCESSION AA475936  
VERSION AA475936.1 GI:2203787  
KEYWORDS EST  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 76)  
AUTHORS Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,  
Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,  
Schellenberg K., Seftoe M., Tan F., Underwood K., Moore B.,  
Theising B., Wylie T., Lennon G., Soares B., Wilson R. and  
Waterston R.

TITLE The WashU-HHMI Mouse EST Project  
JOURNAL Unpublished  
COMMENT Contact: Marra M/Mouse EST Project  
WashU-HHMI Mouse EST Project  
Washington University School of MedicineP  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MG1:515955

Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -28m13 rev2 ET from Amersham  
High quality sequence stop: 1.

FEATURES  
source Location/Qualifiers  
1..76  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:876475"  
/sex="male"  
/tissue\_type="mammary gland"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"  
/clone\_lib="Soares\_mammary\_gland\_NbMMG"  
/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia  
Ri; with a modified polylinker; Site 1: Not I; Site 2: Eco  
Ri; 1st strand cDNA was primed with a Not I - oligo(dT)  
primer [5',  
TGTTCACCAATCTCAAGTCGAGCGCGCGCAATGCTTTTTTTTTTTTTTTTTT  
T 3'). double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT7T3 vector.  
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library  
constructed and normalized by Bento Soares and M.Fatima

BASE COUNT 21 a 11 c 10 g 16 t

ORIGIN

Query Match 52.6%; Score 10; DB 29; Length 58;  
Best Local Similarity 52.6%; Pred. No. 2.3e+04;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19  
|||||

Db 34 CCAATCTGTGTAGCCACG 16  
|||||

BASE COUNT 19 a 28 c 16 g 13 t

ORIGIN

Query Match 52.6%; Score 10; DB 9; Length 76;  
Best Local Similarity 52.6%; Pred. No. 2.5e+04;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19  
|||||

Db 40 CCAATGGTTTAGCCACG 58  
|||||

RESULT 5

LOCUS BQ756881 79 bp mRNA linear EST 26-JUL-2002

DEFINITION EBem09\_SQ005\_E15\_R embryo, 1 Day germination, no treatment, cv

EBem09\_SQ005\_E15 5', mRNA sequence.

ACCESSION BQ756881

VERSION BQ756881.1 GI:21965353

KEYWORDS EST

SOURCE Hordeum vulgare subsp. vulgare

ORGANISM Hordeum vulgare subsp. vulgare

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

SPERMATOPHYTES; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae

1 (bases 1 to 79)

AUTHORS Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardie, L.,

Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.

TITLE Development of Barley Transcriptome Resources

JOURNAL Unpublished

COMMENT Contact: Waugh R. Marshall DF

Genome Dynamics/Computational Biology

Scottish Crop Research Institute

Invergowrie, Dundee, DD2 5DA, Scotland, UK

Tel: 00 44 1382 562731

Fax: 00 44 1382 562426

Email: est@scri.sari.ac.uk

FEATURES  
source Location/Qualifiers  
1..79  
/organism="Hordeum vulgare subsp. vulgare"  
/mol\_type="mRNA"  
/cultivar="Optic"  
/db\_xref="taxon:112509"  
/clone="EBem09\_SQ005\_E15"  
/tissue\_type="embryo"  
/dev\_stage="1 Day germination"  
/lab\_host="DH10B"  
/clone\_lib="embryo, 1 Day germination, no treatment, cv  
Optic\_EBem09"  
/note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;  
Non-normalised library, directionally cloned into pSPORT1.  
Derived from embryos dissected from germinating grains (1  
day) in glasshouse grown barley plants. Developed as part  
of the barley transcriptome resources of BBSRC/SEERAD  
funded cereal IGF (Investigating Gene Function) project."

BASE COUNT 19 a 18 c 17 g 25 t

ORIGIN

Query Match 52.6%; Score 10; DB 13; Length 79;  
Best Local Similarity 52.6%; Pred. No. 2.6e+04;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19  
|||||

Db 42 CCAATTTTGTCAACACG 60  
|||||

RESULT 6

LOCUS AL897168 80 bp mRNA linear EST 16-SEP-2002

DEFINITION AL897168 XGC-egg Silurana tropicalis cDNA clone TEGg01ld06 3', mRNA

```

sequence.
ACCESSION      AL897168
VERSION        AL897168.1  GI:22949622
SOURCE         EST.
ORGANISM       Silurana tropicalis (western clawed frog)
               Silurana tropicalis
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
               Xenopodinae; Silurana.
               1 (bases 1 to 80)
REFERENCE      Taylor,R., Ashurst,J.L., Croning,M.D.R., Zorn,A.M. and Rogers,J.
TITLE          Sanger Xenopus tropicalis EST project 2002
JOURNAL        Unpublished
COMMENT        Contact: Taylor R
               Sanger Centre
               Hinxton, Cambridgeshire, CB10 1SA, UK
               Email: trop@sanger.ac.uk
               Sanger Xenopus tropicalis EST project 2001
               TROPICALIS_SEQUENCE_ID: TEGG01ld06.q1kT7
               Sequencing primer: T7
               This sequence is from a Xenopus Gene Collection (XGC) library
               constructed by Aaron M. Zorn.
FEATURES       Location/Qualifiers
               1..80
               /organism="Silurana tropicalis"
               /mol_type="mRNA"
               /db_xref="taxon:8364"
               /clone="TEGG01ld06"
               /dev_stage="egg"
               /lab_host="Escherichia coli XL1-blue"
               /clone_lib="XGC-egg"
               /note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
               was oligo dt primed from 5ug of poly A+ RNA from egg.
               EcoRI-NotI cut cDNA was then ligated into pCS107 with
               EcoRI at the 5' end and NotI at the 3' end"
BASE COUNT    17 a 12 c 14 g 37 t
ORIGIN
Query Match      52.6%; Score 10; DB 9; Length 80;
Best Local Similarity 52.6%; Pred. No. 2.6e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
    |||||
Db 71 CCAATCGTAAATGTCACG 53
    |||||

RESULT 7
BH251489/c
LOCUS          BH251489
DEFINITION     SALK_011672 Arabidopsis thaliana TDNA insertion lines Arabidopsis
               thaliana genomic clone SALK_011672, genomic survey sequence.
ACCESSION      BH251489.1  GI:17138467
VERSION        BH251489
KEYWORDS       GSS.
SOURCE         Arabidopsis thaliana (thale cress)
ORGANISM       Arabidopsis thaliana
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
               ; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
               1 (bases 1 to 80)
REFERENCE      Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
               ,C., Jecke,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
               , Zimmerman,J. and Ecker,J.R.
AUTHORS        A Sequence-Indexed Library of Insertion Mutations in the
               Arabidopsis Genome
JOURNAL        Unpublished
COMMENT        Contact: Joseph R. Ecker
               Salk Institute Genomic Analysis Laboratory (SIGNAL)
               The Salk Institute for Biological Studies
               10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
               Tel: 858 453 4100 x1752
               Fax: 858 558 6379

Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..80
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_011672"
/notes="PCR was performed on Arabidopsis thaliana TDNA insertion lines"
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT    18 a 20 c 21 g 19 t 2 others
ORIGIN
Query Match      52.6%; Score 10; DB 28; Length 80;
Best Local Similarity 52.6%; Pred. No. 2.6e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
    |||||
Db 26 CCAATGATAAATAGCCACG 8
    |||||

RESULT 8
BQ099298
LOCUS          BQ099298
DEFINITION     ph28h02.y2 Ostertagia ostertagi L3 pAMP1 v1 Ostertagia ostertagi
               cDNA 5', mRNA sequence.
ACCESSION      BQ099298
VERSION        BQ099298.1  GI:20132282
KEYWORDS       EST.
SOURCE         Ostertagia ostertagi
ORGANISM       Ostertagia ostertagi
               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
               Trichostrongyloidea; Haemonchidae; Ostertagiinae; Ostertagia.
               1 (bases 1 to 82)
REFERENCE      McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.
               , Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.
               , Gibbons,M., Ritter,S., Bennett,J., Franklin,C., Teagareishvili,R.
               , Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
               ,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.
               , Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
               Wilson,R.
AUTHORS        The Washington Univ. Nematode EST Project, 1999
               Unpublished
TITLE          McCarter JP
JOURNAL        The Washington Univ. Nematode EST Project, 1999
COMMENT        Washington University School of Medicine
               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
               Tel: 314 286 1800
               Fax: 314 286 1810
               Email: est@wustl.wustl.edu
               The library was constructed by Claire Murphy and Dr. James McCarter
               at Washington University, St. Louis. DNA Sequencing by: Washington
               University Genome Sequencing Center
               High quality sequence stop: 69.
               Location/Qualifiers
               1..82
               /organism="Ostertagia ostertagi"
               /mol_type="mRNA"
               /db_xref="taxon:6317"
               /dev_stage="L3"
               /lab_host="DH10B"
               /clone_lib="Ostertagia ostertagi L3 pAMP1 v1"
               /note="Vector: pAMP1 (Gibco); Site_1: NotI; Site_2: SalI;
               ***WARNING: Subsequent examination of these samples has

```

revealed the presence of an additional Trichostrongyloidea cattle nematode, Cooperia oncophora. Sequences in this library may derive from either Ostertagia or Cooperia.\*\*\* The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Nematodes were provided by Dr. Louis Gasbarre of the USDA, Beltsville, MD (lgasbarre@nri.barc.usda.gov). Third stage exsheathed larvae were collected from 14 day fecal-sphagnum moss cultures of Ostertagia eggs. The larvae were recovered by overnight passage on a Baermann apparatus, and then cleaned by passage through a 20 micron nylon mesh. The larvae were then subjected to a treatment with 1.25% chlorox to induce excystation. The larvae were washed with 5 changes of PBS and then pelleted and snap frozen in liquid nitrogen."

BASE COUNT 24 a 24 c 12 g 22 t  
ORIGIN

Query Match 52.6%; Score 10; DB 13; Length 82;  
Best Local Similarity 52.6%; Pred. No. 2.6e+04;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNCCACG 19  
|||||  
Db 12 CCAATGGAGAGTGTCACG 30

RESULT 9  
BH232183/c  
LOCUS  
DEFINITION 86 bp DNA linear GSS 08-NOV-2001  
survey sequence.  
ACCESSION BH232183 GI:16837119  
VERSION  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 86)  
Walbot,V.  
Maize genomic sequences found using engineered RescueMu transposon

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Contact: Walbot V  
Unpublished  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Possible ligation site so sequence was trimmed. Post-ligation sequence submitted separately.  
Plate: 1006166 row: 23  
Class: transposon-tagged.  
Location/Qualifiers  
1. .86  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1006 - RescueMu Grid G"  
/notes="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA."

BASE COUNT 11 a 27 c 44 g 15 t  
ORIGIN

Query Match 52.6%; Score 10; DB 28; Length 97;  
Best Local Similarity 52.6%; Pred. No. 2.8e+04;

Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 13 a 24 c 37 g 12 t  
ORIGIN

Query Match 52.6%; Score 10; DB 28; Length 86;  
Best Local Similarity 52.6%; Pred. No. 2.6e+04;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNCCACG 19  
|||||  
Db 61 CCAATCATTTGGAGCCACG 43

RESULT 10  
BH222106/c  
LOCUS  
DEFINITION 97 bp DNA linear GSS 08-NOV-2001  
survey sequence.  
ACCESSION BH222106 GI:16816606  
VERSION  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 97)  
Walbot,V.  
Maize genomic sequences found using engineered RescueMu transposon

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Contact: Walbot V  
Unpublished  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 1006105 row: 13  
Class: transposon-tagged.  
Location/Qualifiers  
1. .97  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1006 - RescueMu Grid G"  
/notes="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA."  
Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 11 a 27 c 44 g 15 t  
ORIGIN

Query Match 52.6%; Score 10; DB 28; Length 97;  
Best Local Similarity 52.6%; Pred. No. 2.8e+04;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNCCACG 19  
 |||||  
 Db 92 CCAATTCGAGCACCACG 74

## RESULT 11

CB338675/c

## LOCUS

DEFINITION CB338675 99 bp mRNA linear EST 13-MAR-2003  
 kb59b04.y1 Brugia malayi L3 pAMP1 v2 Brugia malayi cDNA 5' similar  
 to TR:O16159 O16159 CYSTATIN-TYPE CYSTEINE PROTEINASE INHIBITOR. ;,  
 mRNA sequence.

## ACCESSION

CB338675

## VERSION

CB338675.1

## KEYWORDS

GI:28941376

## SOURCE

Brugia malayi

## ORGANISM

Brugia malayi

## REFERENCE

1 (bases 1 to 99)

## AUTHORS

McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.,  
 Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,  
 Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Teagareishvili,R.,  
 Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe  
 M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,  
 Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and  
 Wilson,R.

## TITLE

The Washington Univ. Nematode EST Project, 1999

## JOURNAL

Unpublished

## COMMENT

Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Nematodes were provided by Dr. Ben-Wen Li and Dr. Gary Weil of

Washington University, St. Louis, MO (weillab@ingate.wustl.edu).

Seq primer: -40RP from Gibco.

## FEATURES

Location/Qualifiers

1..99

/organism="Brugia malayi"

/mol\_type="mRNA"

/db\_xref="taxon:6279"

/dev\_stage="L3"

/lab\_host="DH10B"

/clone\_lib="Brugia malayi L3 pAMP1 v2"

/notes="Vector: pAMP1(Invitrogen); Site.1: NotI; Site.2:  
 SalI; The library was constructed by Amy Rush, Claire  
 Murphy and Dr. James McCarter at Washington University,  
 St. Louis. The cDNA was made by using Dynabead oligo-dT  
 priming (Dyna). PCR based library using a modified  
 protocol from the SMART PCR cDNA Synthesis Kit from  
 Clontech. Directionally cloned into the UDG sites of  
 pAMP1. Nematodes were provided by Dr. Ben-Wen Li and Dr.  
 Gary Weil of Washington University, St. Louis, MO  
 (weillab@ingate.wustl.edu)."

BASE COUNT 31 a 16 c 21 g 31 t

## ORIGIN

Query Match 52.6%; Score 10; DB 14; Length 99;

Best Local Similarity 52.6%; Pred. No. 2.8e+04;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNCCACG 19

|||||

Db 97 CCAATAAACTTGGCCACG 79

## RESULT 12

AZ921866/c

## LOCUS

AZ921866

99 bp DNA linear GSS 07-JUN-2002

## DEFINITION

HRCot4D10 Sorghum bicolor HRCot Sorghum bicolor genomic, genomic

survey sequence.

ACCESSION AZ921866

VERSION AZ921866.1

KEYWORDS GI:13400225

SOURCE GSS.

ORGANISM Sorghum bicolor (sorghum)

## REFERENCE

1 (bases 1 to 99)

## AUTHORS

Peterson,D.G., Schulze,S.R., Sciara,E.B., Lee,S.A., Bowers,J.E.,  
 Nagel,A., Jiang,N., Tibbitts,D.C., Wessler,S.R. and Paterson,A.H.

## TITLE

Integration of Cot analysis, DNA cloning, and high-throughput

sequencing facilitates genome characterization and gene discovery

Genome Res. 12 (5), 795-807 (2002)

## JOURNAL

MEDLINE 21992826

## PUBMED

11997346

## COMMENT

Contact: Peterson DG

Plant Genome Mapping Laboratory

University of Georgia

Room 162, Riverbend Research Bldg., 110 Riverbend Rd., Athens, GA

30602, USA

Tel: 706-583-0167

Fax: 706-583-0160

Email: dgsearches.uga.edu

Class: Hydroxyapatite-fractionated DNA.

## FEATURES

Location/Qualifiers

1..99

/organism="Sorghum bicolor"

/mol\_type="genomic DNA"

/cultivar="BTx623"

/db\_xref="taxon:4558"

/tissue\_type="leaves"

/dev\_stage="seedling"

/clone\_lib="Sorghum bicolor HRCot"

/notes="Vector: pGEM-TA-Easy; A Cot analysis was performed

for the sorghum genome. Based on the resulting Cot curve,

hydroxyapatite chromatography was used to isolate

'highly-repetitive' (HR), 'moderately-repetitive' (MR),

and 'single/low-copy' (SL) sequence components from

sheared genomic DNA. The three repetition-based DNA

components were cloned into E. coli to produce HRCot,

MRCot, and SiCot genomic libraries. Blotting and

sequencing data indicates that each library is

representative of the component from which it was derived.

Putative ID listings given for sequences are based on

comparison (blastn) with sequences in the NCBI Nr

Database. Only the primary match is given (all primary E

values are &lt; or = 1.00E-5). In no instance does a 'Cot

clone' contain the complete sequence of its putative Nr

match."

BASE COUNT 18 a 19 c 29 g 33 t

## ORIGIN

Query Match 52.6%; Score 10; DB 28; Length 99;

Best Local Similarity 52.6%; Pred. No. 2.8e+04;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNCCACG 19

|||||

Db 56 CCAATTGCATCTCCACG 38

Survey sequence.

ACCESSION AZ921866

VERSION AZ921866.1

KEYWORDS GI:13400225

SOURCE GSS.

ORGANISM Sorghum bicolor (sorghum)

Sorghum bicolor

1 (bases 1 to 99)

Peterson,D.G., Schulze,S.R., Sciara,E.B., Lee,S.A., Bowers,J.E.,

Nagel,A., Jiang,N., Tibbitts,D.C., Wessler,S.R. and Paterson,A.H.

Integration of Cot analysis, DNA cloning, and high-throughput

sequencing facilitates genome characterization and gene discovery

Genome Res. 12 (5), 795-807 (2002)

21992826

11997346

Contact: Peterson DG

Plant Genome Mapping Laboratory

University of Georgia

Room 162, Riverbend Research Bldg., 110 Riverbend Rd., Athens, GA

30602, USA

Tel: 706-583-0167

Fax: 706-583-0160

Email: dgsearches.uga.edu

Class: Hydroxyapatite-fractionated DNA.

Location/Qualifiers

1..99

/organism="Sorghum bicolor"

/mol\_type="genomic DNA"

/cultivar="BTx623"

/db\_xref="taxon:4558"

/tissue\_type="leaves"

/dev\_stage="seedling"

/clone\_lib="Sorghum bicolor HRCot"

/notes="Vector: pGEM-TA-Easy; A Cot analysis was performed

for the sorghum genome. Based on the resulting Cot curve,

hydroxyapatite chromatography was used to isolate

'highly-repetitive' (HR), 'moderately-repetitive' (MR),

and 'single/low-copy' (SL) sequence components from

sheared genomic DNA. The three repetition-based DNA

components were cloned into E. coli to produce HRCot,

MRCot, and SiCot genomic libraries. Blotting and

sequencing data indicates that each library is

representative of the component from which it was derived.

Putative ID listings given for sequences are based on

comparison (blastn) with sequences in the NCBI Nr

Database. Only the primary match is given (all primary E

values are < or = 1.00E-5). In no instance does a 'Cot

clone' contain the complete sequence of its putative Nr

match."

BASE COUNT 18 a 19 c 29 g 33 t

ORIGIN

Query Match 52.6%; Score 10; DB 28; Length 99;

Best Local Similarity 52.6%; Pred. No. 2.8e+04;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNCCACG 19

|||||

Db 56 CCAATTGCATCTCCACG 38

BF086094

CM3-GN0052-080900-334-cl1 GN0052 Homo sapiens cDNA, mRNA sequence.

100 bp mRNA linear EST 19-OCT-2000

BF086094

BF086094.1

GI:10891804

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

#### REFERENCE AUTHORS

1 (bases 1 to 100)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

#### TITLE

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

#### JOURNAL MEDLINE PUBMED COMMENT

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=kt2-cm3-GN0052-080>)

900-334-cl1kt3=2000-09-08&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 5

High quality sequence stop: 100.

#### FEATURES source

1..100  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="GN0052"  
/note="Organ: placenta normal; Vector: puc18; Site 1: SmaI  
; Site 2: SmaI; A mini-library was made by cloning  
products derived from ORESTES PCR (U.S. Letters Patent  
application No. 196,716 - Ludwig Institute for Cancer  
Research) profiles into the pUC 18 vector. Reverse  
transcription of tissue mRNA and cDNA amplification were  
performed under low stringency conditions."

#### BASE COUNT ORIGIN

35 a 23 c 18 g 24 t  
Query Match 52.6%; Score 10; DB 10; Length 100;  
Best Local Similarity 52.6%; Pred. No. 2.8e+04;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19  
||||| |||||  
DB 82 CCAATTCTCGAATCCACG 100

#### RESULT 14 BH583741

LOCUS BOGXN16TR BOGX Brassica oleracea genomic clone BOGXN16, genomic  
survey sequence.  
DEFINITION BH583741

ACCSSION BH583741

VERSION BH583741.1 GI:17836198

KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids II; Brassicales; Brassicaceae; Brassica.

#### REFERENCE

1 (bases 1 to 101)  
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.

Whole genome shotgun sequencing of Brassica oleracea

#### TITLE

#### JOURNAL

#### COMMENT

Unpublished  
Contact: Chris Town

#### TIGR

7112 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: sheared ends

Location/Qualifiers

1..101  
/organism="Brassica oleracea"  
/mol\_type="genomic DNA"  
/strain="TO1000DH3"  
/db\_xref="taxon:3712"  
/clone\_lib="BOGXN16"  
/notes="vector: PHOS1; Site 1: BstXI; 2-3 kb sheared  
genomic DNA inserted into PHOS1 using BstXI linkers"

#### BASE COUNT ORIGIN

38 a 23 c 22 g 18 t  
Query Match 52.6%; Score 10; DB 28; Length 101;  
Best Local Similarity 52.6%; Pred. No. 2.8e+04;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19

||||| |||||

DB 25 CCAATCGCGGCCGCCACG 43

#### RESULT 15 AA927925/c

#### LOCUS

#### DEFINITION

AA927925

AA927925.1

GI:3076669

EST.

Homo sapiens

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

Insert Length: 553 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 57.

#### FEATURES source

1..103  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1541833"  
/lab\_host="DH10B"  
/clone\_lib="Soares NFL T\_GBC\_S1"  
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with  
a modified polylinker; Site 1: Not I; Site 2: Eco RI;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung NBHL19W, testis NHT, and B-cell  
NCI CGAP GCBI) were mixed, and as circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento

BASE COUNT 25 a 23 c 25 g 30 t  
ORIGIN Soares and M. Fatima Bonaldo. "

Query Match 52.6%; Score 10; DB 9; Length 103;  
Best Local Similarity 52.6%; Pred. No. 2.8e+04;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNCCACG 19  
| | | | |  
Db 55 CCAATTCATCGGACCACG 37  
| | | | |

Search completed: December 4, 2003, 09:57:25  
Job time : 2150 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 05:16:13 ; Search time 1492 Seconds  
(without alignments)  
520.967 Million cell updates/sec

Title: US-09-606-804-1

Perfect score: 19  
Sequence: 1 ccaatnnnnnnnnccacg 19

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

1: gb\_ba.\*  
2: gb\_hcg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
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7: gb\_ph.\*  
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14: gb\_vi.\*  
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23: em\_pat.\*  
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30: em\_htg\_hum.\*  
31: em\_htg\_inv.\*  
32: em\_htg\_other.\*  
33: em\_htg\_mus.\*  
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35: em\_htg\_rod.\*  
36: em\_htg\_mam.\*  
37: em\_htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match %	Query Length	DB ID	Description
1	10	52.6	19	6	AR274677 Sequence
2	10	52.6	19	6	AX275341 Sequence
3	10	52.6	19	6	BD016693 Method fo
4	10	52.6	19	6	E28797 Endoplasmic
5	10	52.6	19	6	E28801 Endoplasmic
6	10	52.6	19	6	E28802 Endoplasmic
7	10	52.6	19	6	E28803 Endoplasmic
8	10	52.6	19	6	E28804 Endoplasmic
9	10	52.6	19	6	E28805 Endoplasmic
10	10	52.6	19	6	E28806 Endoplasmic
11	10	52.6	19	6	E28807 Endoplasmic
12	10	52.6	19	6	E28808 Endoplasmic
13	10	52.6	19	6	E28809 Endoplasmic
14	10	52.6	19	6	E44202 Endoplasmic
15	10	52.6	19	6	E44206 Endoplasmic
16	10	52.6	19	6	E44207 Endoplasmic
17	10	52.6	19	6	E44208 Endoplasmic
18	10	52.6	19	6	E44209 Endoplasmic
19	10	52.6	19	6	E44210 Endoplasmic
20	10	52.6	19	6	E44211 Endoplasmic
21	10	52.6	19	6	E44212 Endoplasmic
22	10	52.6	19	6	E44213 Endoplasmic
23	10	52.6	19	6	E44214 Endoplasmic
24	10	52.6	24	6	AX443752 Sequence
25	10	52.6	25	6	AX447733 Sequence
26	10	52.6	29	6	E44234 Endoplasmic
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28	10	52.6	99	9	HUMCG3A02
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31	10	52.6	118	8	ATH524636 Arabidops
32	10	52.6	122	6	E28800 Endoplasmic
33	10	52.6	126	6	E44205 Endoplasmic
34	10	52.6	125	14	AF271990 Human ade
35	10	52.6	127	6	AX343728 Sequence
36	10	52.6	133	8	ATH523697 Arabidops
37	10	52.6	136	6	AX033516 Arabidops
38	10	52.6	136	6	AX033517 Sequence
39	10	52.6	138	8	AY203001 Arabidops
40	10	52.6	142	6	AX033504 Sequence
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42	10	52.6	143	9	D10339S05 Homo sapie
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44	10	52.6	145	6	AX072778 Sequence
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# ALIGNMENTS

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AR274677  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

AR274677  
Sequence 1 from patent US 6506600.  
AR274677  
AR274677.1 GI:29707222  
Unknown.  
Unclassified.  
1 (bases 1 to 19)  
Hermonat,P.L., Mane,M. and Liu,Y.  
Secreting products from skin by adeno-associated virus (AAV) gene transfer  
Patent: US 6506600-A 1 14-JAN-2003;

19 bp  
DNA  
linear  
PAT 10-APR-2003

FEATURES  
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BASE COUNT 3 a 5 c 1 g 1 t 9 others  
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AX275341  
LOCUS AX275341 19 bp DNA linear PAT 29-OCT-2001  
DEFINITION Sequence 1 from Patent WO0171018.  
ACCESSION AX275341  
VERSION AX275341.1 GI:16547677  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified.

REFERENCE 1  
AUTHORS Hermonat,P.L., Mane,M. and Liu,Y.  
TITLE Secreting products from skin by adeno-associated virus (aav) gene transfer  
JOURNAL Patent: WO 0171018-A 1 27-SEP-2001;  
THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ARKANSAS (US)

FEATURES  
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Location/Qualifiers  
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Db 1 CCAATNNNNNNNNCCACG 19

RESULT 3  
BD016693  
LOCUS BD016693 19 bp DNA linear PAT 27-AUG-2002  
DEFINITION Method for screening ORP150 expression regulatory substance.  
ACCESSION BD016693  
VERSION BD016693.1 GI:22557869  
KEYWORDS JP 2001238699-A/2.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Akazawa,R., Kaneda,S., Yanagishi,H. and Yura,T.  
TITLE Method for screening ORP150 expression regulatory substance  
JOURNAL Patent: JP 2001238699-A 2 04-SEP-2001;  
HSP RESEARCH INST INC

COMMENT OS Artificial Sequence  
PN JP 2001238699-A/2  
PD 04-SEP-2001  
PF 01-MAR-2000 JP 2000055384  
PI RIEKO AKAZAWA, SUMIKO KANEDA, HIDEKI YANAGI, TAKASHI YURA PC  
C1201/68,A61K45/00,A61P3/10,A61P9/10,A61P17/02,A61P25/ PC  
28,  
PC A61P35/00,A61P37/00,C12N5/10,C12N15/09/(C12N5/10,C12R1:91),  
PC (C12N15/09,C12R1:91),C12N5/00,C12N15/00,(C12N5/00,C12R1:91),

PC (C12N15/00,C12R1:91)  
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CC is ERSE consensus sequence.  
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Best Local Similarity 100.0%; Pred. No. 2.7e+04;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CCAATNNNNNNNNCCACG 19

RESULT 4  
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LOCUS E28797 19 bp DNA linear PAT 18-JUN-2001  
DEFINITION Endoplasmic reticulum stress-response regulatory element.  
ACCESSION E28797  
VERSION E28797.1 GI:13020851  
KEYWORDS JP 1999243959-A/1.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Hideo,Y., Hideki,Y. and Takashi,Y.  
TITLE Endoplasmic reticulum stress-response regulatory element  
JOURNAL Patent: JP 1999243959-A 1 14-SEP-1999;  
HSP RESEARCH INST INC

COMMENT OS Unidentified  
PN JP 1999243959-A/1  
PD 14-SEP-1999  
PF 04-MAR-1998 JP 1998052453  
PR HIDEO YOSHIDA,HIDEKI YANAGI,TAKASHI YURA  
PC C12N15/09,A61K35/74,A61K35/76,A61K38/00,A61K48/00,C12N15/00,  
PC A61K37/02  
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CC Topology: Linear;  
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Best Local Similarity 100.0%; Pred. No. 2.7e+04;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Endoplasmic reticulum stress-response regulatory element.  
ACCESSION E28801  
VERSION E28801.1 GI:13020855

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KEYWORDS      JP 199243959-A/5.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1. (bases 1 to 19)
AUTHORS      Hideo,Y., Hideki,Y. and Takashi,Y.
TITLE        Endoplasmic reticulum stress-response regulatory element
JOURNAL      Patent: JP 199243959-A 5 14-SEP-1999;
              HSP RESEARCH INST INC
COMMENT      OS Homo sapiens (human)
              PN JP 199243959-A/5
              PD 14-SEP-1999
              PF 04-MAR-1998 JP 1998052453
              PR HIDEO YOSHIDA,HIDEKI YANAGI,TAKASHI YURA
              PC C12N15/09,A61K35/74,A61K35/76,A61K38/00,C12N15/00,
              PC A61K37/02
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              CC Topology: Linear;
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BASE COUNT   3 a 9 c 5 g
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Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 1 CCAATCGCGCGCTCCACG 19

RESULT 6
LOCUS      E28802      19 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Endoplasmic reticulum stress-response regulatory element.
ACCESSION  E28802
VERSION     E28802.1 GI:13020856
KEYWORDS   JP 199243959-A/6.
SOURCE     Mus sp.
ORGANISM   Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Hideo,Y., Hideki,Y. and Takashi,Y.
Endoplasmic reticulum stress-response regulatory element
Patent: JP 199243959-A 6 14-SEP-1999;
HSP RESEARCH INST INC
OS Mus sp. (mouse)
PN JP 199243959-A/6
PD 14-SEP-1999
PF 04-MAR-1998 JP 1998052453
PR HIDEO YOSHIDA,HIDEKI YANAGI,TAKASHI YURA
PC C12N15/09,A61K35/74,A61K35/76,A61K38/00,A61K48/00,C12N15/00,
PC A61K37/02
CC Strandedness: Double;
CC Topology: Linear;
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Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 1 CCAATCGCGCGCTCCACG 19

RESULT 7
LOCUS      E28803      19 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Endoplasmic reticulum stress-response regulatory element.
ACCESSION  E28803
VERSION     E28803.1 GI:13020857
KEYWORDS   JP 199243959-A/7.
SOURCE     Rattus sp.
ORGANISM   Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 19)
Hideo,Y., Hideki,Y. and Takashi,Y.
Endoplasmic reticulum stress-response regulatory element
Patent: JP 199243959-A 7 14-SEP-1999;
HSP RESEARCH INST INC
OS Rattus sp. (rat)
PN JP 199243959-A/7
PD 14-SEP-1999
PF 04-MAR-1998 JP 1998052453
PR HIDEO YOSHIDA,HIDEKI YANAGI,TAKASHI YURA
PC C12N15/09,A61K35/74,A61K35/76,A61K38/00,A61K48/00,C12N15/00,
PC A61K37/02
CC Strandedness: Double;
CC Topology: Linear;
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BASE COUNT   4 a 8 c 5 g
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Best Local Similarity 52.6%; Pred. No. 2.7e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
Db 1 CCAATCGCGCGCTCCACG 19

RESULT 8
LOCUS      E28804      19 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Endoplasmic reticulum stress-response regulatory element.
ACCESSION  E28804
VERSION     E28804.1 GI:13020858
KEYWORDS   JP 199243959-A/8.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
Hideo,Y., Hideki,Y. and Takashi,Y.
Endoplasmic reticulum stress-response regulatory element
Patent: JP 199243959-A 8 14-SEP-1999;
HSP RESEARCH INST INC
```

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COMMENT      OS      Homo sapiens (human)
PN      JP 1999243959-A/8
PD      14-SEP-1999
PF      04-MAR-1998 JP 1998052453
PR      HIDEO YOSHIDA,HIDEKI YANAGI,TAKASHI YURA
PI      C12N15/09,A61K35/74,A61K35/76,A61K38/00,A61K48/00,C12N15/00,
PC      A61K37/02
CC      Strandedness: Double;
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Best Local Similarity 52.6%; Pred. No. 2.7e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      1 CCAATNNNNNNNNCCACG 19
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Db      1 CCAATCGGCGCCACCACG 19
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RESULT 9
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LOCUS      19 bp DNA linear PAT 18-JUN-2001
DEFINITION Endoplasmic reticulum stress-response regulatory element.
ACCESSION E28805
VERSION JP 1999243959-A/9.
KEYWORDS Gallus sp.
ORGANISM Gallus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 19)
Hideo,Y., Hideki,Y. and Takashi,Y.
Endoplasmic reticulum stress-response regulatory element
Patent: JP 1999243959-A 9 14-SEP-1999;
HSP RESEARCH INST INC
OS Gallus sp. (chicken)
PN JP 1999243959-A/9
PD 14-SEP-1999
PF 04-MAR-1998 JP 1998052453
PR HIDEO YOSHIDA,HIDEKI YANAGI,TAKASHI YURA
PI C12N15/09,A61K35/74,A61K35/76,A61K38/00,A61K48/00,C12N15/00,
PC A61K37/02
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CC Topology: Linear;
FH Key      Location/Qualifiers
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Db      1 CCAATGGGAGCGCACCACG 19
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RESULT 10
E28806
LOCUS      19 bp DNA linear PAT 18-JUN-2001
DEFINITION Endoplasmic reticulum stress-response regulatory element.
ACCESSION E28806
VERSION JP 1999243959-A/10.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
Hideo,Y., Hideki,Y. and Takashi,Y.
Endoplasmic reticulum stress-response regulatory element
Patent: JP 1999243959-A 10 14-SEP-1999;
HSP RESEARCH INST INC
OS Homo sapiens (human)
PN JP 1999243959-A/10
PD 14-SEP-1999
PF 04-MAR-1998 JP 1998052453
PR HIDEO YOSHIDA,HIDEKI YANAGI,TAKASHI YURA
PI C12N15/09,A61K35/74,A61K35/76,A61K38/00,A61K48/00,C12N15/00,
PC A61K37/02
CC Strandedness: Double;
CC Topology: Linear;
FH Key      Location/Qualifiers
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Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      1 CCAATNNNNNNNNCCACG 19
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Db      1 CCAATCGGAGGAGCCACG 19
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RESULT 11
E28807
LOCUS      19 bp DNA linear PAT 18-JUN-2001
DEFINITION Endoplasmic reticulum stress-response regulatory element.
ACCESSION E28807
VERSION JP 1999243959-A/11.
KEYWORDS Gallus sp.
SOURCE Gallus sp.
ORGANISM Gallus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 19)
Hideo,Y., Hideki,Y. and Takashi,Y.
Endoplasmic reticulum stress-response regulatory element
Patent: JP 1999243959-A 11 14-SEP-1999;
HSP RESEARCH INST INC
OS Gallus sp. (chicken)
PN JP 1999243959-A/11
PD 14-SEP-1999
PF 04-MAR-1998 JP 1998052453
PR HIDEO YOSHIDA,HIDEKI YANAGI,TAKASHI YURA
PI C12N15/09,A61K35/74,A61K35/76,A61K38/00,A61K48/00,C12N15/00,
PC A61K37/02
CC Strandedness: Double;

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CC Topology: Linear;
FH Key Location/Qualifiers
FT enhancer 1..19.
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BASE COUNT      4 a 9 c 5 g 1 t
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Best Local Similarity 52.6%; Pred. No. 2.7e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
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Db 1 CCAATCGACGCCGCCACG 19
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RESULT 12
E28808
LOCUS      E28808      19 bp DNA linear PAT 18-JUN-2001
DEFINITION Endoplasmic reticulum stress-response regulatory element.
ACCESSION E28808
VERSION E28808.1 GI:13020862
KEYWORDS JP 1999243959-A/12.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
Hideo,Y., Hideo,Y. and Takashi,Y.
Patent: JP 1999243959-A 12 14-SEP-1999;
HSP RESEARCH INST INC
OS Homo sapiens (human)
PN JP 1999243959-A/12
PD 14-SEP-1999
PF 04-MAR-1998 JP 1998052453
PR HIDEO YOSHIDA,HIDEKI YANAGI,TAKASHI YURA
PC C12N15/09,A61K35/74,A61K38/00,A61K48/00,C12N15/00,
PC A61K37/02
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT enhancer 1..19.
FEATURES
    source
        Location/Qualifiers
            1..19
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT      5 a 6 c 5 g 3 t
ORIGIN
Query Match      52.6%; Score 10; DB 6; Length 19;
Best Local Similarity 52.6%; Pred. No. 2.7e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
    |||||
Db 1 CCAATGATGTCGACCACG 19
    |||||

RESULT 13
E28809
LOCUS      E28809      19 bp DNA linear PAT 18-JUN-2001
DEFINITION Endoplasmic reticulum stress-response regulatory element.
ACCESSION E28809
VERSION E28809.1 GI:13020863
KEYWORDS JP 1999243959-A/13.
SOURCE Mus sp.

```

```

ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Hideo,Y., Hideo,Y. and Takashi,Y.
Patent: JP 1999243959-A 13 14-SEP-1999;
HSP RESEARCH INST INC
OS Mus sp. (mouse)
PN JP 1999243959-A/13
PD 14-SEP-1999
PF 04-MAR-1998 JP 1998052453
PR HIDEO YOSHIDA,HIDEKI YANAGI,TAKASHI YURA
PC C12N15/09,A61K35/74,A61K38/00,A61K48/00,C12N15/00,
PC A61K37/02
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT enhancer 1..19.
FEATURES
    source
        Location/Qualifiers
            1..19
            /organism="Mus sp."
            /mol_type="genomic DNA"
            /db_xref="taxon:10095"
BASE COUNT      5 a 6 c 6 g 2 t
ORIGIN
Query Match      52.6%; Score 10; DB 6; Length 19;
Best Local Similarity 52.6%; Pred. No. 2.7e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
    |||||
Db 1 CCAATGAGGTCGACCACG 19
    |||||

RESULT 14
E44202
LOCUS      E44202      19 bp DNA linear PAT 31-JAN-2002
DEFINITION Endoplasmic reticulum stress transcription factor.
ACCESSION E44202
VERSION E44202.1 GI:18633455
KEYWORDS JP 2001054391-A/1.
SOURCE synthetic construct
ORGANISM artificial sequences.
1 (bases 1 to 19)
Haji,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.
Patent: JP 2001054391-A 1 27-FEB-2001;
HSP RESEARCH INST INC
OS Artificial Sequence
PN JP 2001054391-A/1
PD 27-FEB-2001
PF 11-NOV-1999 JP 1999321743
PR KYOSUKE HAJI,HIDEO YOSHIDA,KAZUTOSHI MORI,HIDEKI YANAGI, PI
TAKASHI YURA
PC C12N15/09,C12P21/02,/(C12N15/09,C12R1:91),C12N15/00,(C12N15/00,PC
C12R1:91)
CC
FH Key Location/Qualifiers
FT source 1..19
    /organism='Artificial Sequence'.
FEATURES
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        Location/Qualifiers
            1..19
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BASE COUNT      3 a 5 c 1 g 1 t 9 others
ORIGIN

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Query Match 52.6%; Score 10; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.7e+04;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19  
|||||  
Db 1 CCAATNNNNNNNNCCACG 19

RESULT 15

E44206 19 bp DNA linear PAT 31-JAN-2002  
LOCUS Endoplasmic reticulum stress transcription factor.  
DEFINITION  
E44206  
E44206.1 GI:18633459  
VERSION JP 2001054391-A/5.  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
Haji,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.  
Endoplasmic reticulum stress transcription factor  
Patent: JP 2001054391-A 5 27-FEB-2001;  
JOURNAL HSP RESEARCH INST INC

COMMENT  
OS Homo sapiens (human)  
PN JP 2001054391-A/5  
PD 27-FEB-2001  
PF 11-NOV-1999 JP 1999321743

PR  
PI KYOSUKE HAJI,HIDEO YOSHIDA,KAZUTOSHI MORI,HIDEKI YANAGI, PI  
TAKASHI YURA  
PC  
C12N15/09,C12P21/02//(C12N15/09,C12R1:91),C12N15/00,(C12N15/00, PC  
C12R1:91)

CC  
FH Key Location/Qualifiers  
FT source 1..19 /organism='Homo sapiens (human)'.  
FEATURES  
source  
1..19  
/organism='Homo sapiens'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:9606'

BASE COUNT 3 a 9 c 5 g 2 t  
ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;  
Best Local Similarity 52.6%; Pred. No. 2.7e+04;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19  
|||||  
Db 1 CCAATCGCGGCTCCACG 19

Search completed: December 4, 2003, 07:13:02  
Job time : 1495 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 04:27:16 ; Search time 256 Seconds  
(without alignments)  
200.349 Million cell updates/sec

Title: US-09-606-804-1

Perfect score: 19  
Sequence: 1 ccaatnnnnnnnnccacg 19

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_19Jun03:\*

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12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.\*  
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24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*  
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	52.6	19	20	AAZ25631
2	10	52.6	19	20	AAZ25632
3	10	52.6	19	20	AAZ25633
4	10	52.6	19	20	AAZ25634
5	10	52.6	19	20	AAZ25635
6	10	52.6	19	20	AAZ25636
7	10	52.6	19	20	AAZ25637
8	10	52.6	19	20	AAZ25638
					Endoplasmic reticu
					Endoplasmic reticu
					Endoplasmic reticu
					Endoplasmic reticu
					Endoplasmic reticu
					Endoplasmic reticu

9	10	52.6	19	20	AAZ25639	Endoplasmic reticu
10	10	52.6	19	20	AAZ25640	Endoplasmic reticu
11	10	52.6	19	21	AAA28570	GRP78 promoter ERS
12	10	52.6	19	21	AAA28571	GRP78 promoter ERS
13	10	52.6	19	21	AAA28572	GRP78 promoter ERS
14	10	52.6	19	21	AAA28573	GRP94 promoter ERS
15	10	52.6	19	21	AAA28574	GRP94 promoter ERS
16	10	52.6	19	21	AAA28575	GRP94 promoter ERS
17	10	52.6	19	21	AAA28576	GRP94 promoter ERS
18	10	52.6	19	21	AAA28577	Calreticulin promo
19	10	52.6	19	21	AAA28578	Calreticulin promo
20	10	52.6	19	21	AAA28579	ERSE consensus se
21	10	52.6	19	22	AAI70001	Endoplasmic respon
22	10	52.6	19	22	AAF28780	GRP78 promoter ERS
23	10	52.6	24	21	AAA28596	Oligonucleotide ad
c 24	10	52.6	24	24	ABQ00200	Oligonucleotide ad
c 25	10	52.6	24	24	ABQ04398	Oligonucleotide ad
c 26	10	52.6	24	24	ABQ04439	Oligonucleotide ad
c 27	10	52.6	24	24	ABQ10685	Oligonucleotide ad
c 28	10	52.6	24	24	ABQ10726	Oligonucleotide ad
c 29	10	52.6	25	19	AAV45529	Helicobacter pylori
c 30	10	52.6	25	24	ABQ12221	Oligonucleotide ad
31	10	52.6	25	24	ABQ12262	Oligonucleotide ad
32	10	52.6	28	21	AAA28597	GRP94 promoter ERS
33	10	52.6	28	21	AAA28599	Calreticulin promo
34	10	52.6	29	21	AAA28602	Tandem repeat comp
35	10	52.6	30	21	AAA28598	GRP94 promoter ERS
36	10	52.6	33	21	AAA28569	GRP78 promoter tan
c 37	10	52.6	50	24	ABZ03658	Human leukocyte ge
38	10	52.6	112	24	ABL41923	Nucleotide sequenc
39	10	52.6	122	20	AAZ25660	Human GRP78 promot
40	10	52.6	122	21	AAZ28566	5' flanking region
41	10	52.6	123	24	ABU60984	Human ovarian canc
42	10	52.6	126	21	AAA71906	IAK fragment NS fr
43	10	52.6	127	24	ABL41924	Nucleotide sequenc
44	10	52.6	143	21	AAA71907	IAK fragment NS fr
c 45	10	52.6	145	22	AAF67488	Novel human polynu

#### ALIGNMENTS

RESULT 1  
AAZ25631  
ID AAZ25631 standard; DNA; 19 BP.  
XX AAZ25631;  
AC AC  
XX 23-DEC-1999 (first entry)  
DT DT  
XX Endoplasmic reticulum stress competence control element SEQ ID NO:1.  
DE Endoplasmic reticulum stress competence control element;  
XX Endoplasmic reticulum; ER; stress competence; control element;  
KW inhibition; growth; apoptosis; cancer; autoimmune disease;  
KW cystic fibrosis; ds.  
XX Homo sapiens.  
OS Homo sapiens.  
XX JF11243959-A.  
PN JF11243959-A.  
XX 14-SEP-1999.  
XX 04-MAR-1998; 98JP-0052453.  
XX 04-MAR-1998; 98JP-0052453.  
PR (HSPK-) HSP KENKYUSHO KK.  
XX WPI; 1999-603708/52.  
XX New control element for stress competence of endoplasmic reticulum -  
PT useful for inhibition of growth and induction of apoptosis in cancer  
PT cells

XX Claim 1; Page 10; 25pp; Japanese.

XX The present invention specifically claims an element shown by: (A) a

CC 19 bp base sequence, CCAATNNNNN NNNCCACG (ERSE); or (B) a modified base

CC sequence having replaced 1-3 bases with the other base(s), which induces

CC transcription with stress on endoplasmic reticulum used for stress

CC competence of endoplasmic reticulum. Also described are: (1) a DNA having

CC transcription inducing activity with stress on endoplasmic reticulum

CC containing the above mentioned element, optionally further containing a

CC promoter DNA; and (2) a vector containing the element optionally with the

CC DNA. The element can be used for the inhibition of growth and induction

CC of apoptosis of cancer cells, and improvement of symptoms of autoimmune

CC diseases and cystic fibrosis by inhibition of autoantibody formation.

XX SQ Sequence 19 BP; 3 A; 5 C; 1 G; 1 T; 9 other;

Query Match 52.6%; Score 10; DB 20; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCAATNNNNN NNNCCACG 19

Db 1 CCAATNNNNN NNNCCACG 19

|||||

RESULT 2

AAZ25632

ID AAZ25632 standard; DNA; 19 BP.

XX AC AAZ25632;

XX DT 23-DEC-1999 (first entry)

XX DE Endoplasmic reticulum stress competence control element SEQ ID NO:5.

XX Endoplasmic reticulum; ER; stress competence; control element;

KW inhibition; growth; apoptosis; cancer; autoimmune disease;

KW cystic fibrosis; ds.

XX Homo sapiens.

XX JP11243959-A.

XX PD 14-SEP-1999.

XX PF 04-MAR-1998; 98JP-0052453.

XX PR 04-MAR-1998; 98JP-0052453.

XX PA (HSPK-) HSP KENKYUSHO KK.

XX WI; 1999-603708/52.

XX New control element for stress competence of endoplasmic reticulum -

PT useful for inhibition of growth and induction of apoptosis in cancer

PT cells

XX Example 1; Fig 3; 25pp; Japanese.

XX The present invention specifically claims an element shown by: (A) a

CC 19 bp base sequence, CCAATNNNNN NNNCCACG (ERSE); or (B) a modified base

CC sequence having replaced 1-3 bases with the other base(s), which induces

CC transcription with stress on endoplasmic reticulum used for stress

CC competence of endoplasmic reticulum. Also described are: (1) a DNA

CC having transcription inducing activity with stress on endoplasmic

CC reticulum containing the above mentioned element, optionally further

CC containing a promoter DNA; and (2) a vector containing the element

CC optionally with the DNA. The element can be used for the inhibition of

CC growth and induction of apoptosis of cancer cells, and improvement of

CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of

CC autoantibody formation. AAZ25632 to AAZ25657 represent elements used in

CC an example from the present invention.

XX SQ Sequence 19 BP; 3 A; 5 C; 2 T; 0 other;

Query Match 52.6%; Score 10; DB 20; Length 19;

Best Local Similarity 52.6%; Pred. No. 1.8e+03;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 1 CCAATNNNNN NNNCCACG 19

Db 1 CCAATCGGCGCTCCACG 19

|||||

RESULT 3

AAZ25633

ID AAZ25633 standard; DNA; 19 BP.

XX AC AAZ25633;

XX DT 23-DEC-1999 (first entry)

XX DE Endoplasmic reticulum stress competence control element SEQ ID NO:6.

XX Endoplasmic reticulum; ER; stress competence; control element;

KW inhibition; growth; apoptosis; cancer; autoimmune disease;

KW cystic fibrosis; ds.

XX Mus sp.

XX JP11243959-A.

XX PD 14-SEP-1999.

XX PF 04-MAR-1998; 98JP-0052453.

XX PR 04-MAR-1998; 98JP-0052453.

XX PA (HSPK-) HSP KENKYUSHO KK.

XX WI; 1999-603708/52.

XX New control element for stress competence of endoplasmic reticulum -

PT useful for inhibition of growth and induction of apoptosis in cancer

PT cells

XX Example 1; Fig 3; 25pp; Japanese.

XX The present invention specifically claims an element shown by: (A) a

CC 19 bp base sequence, CCAATNNNNN NNNCCACG (ERSE); or (B) a modified base

CC sequence having replaced 1-3 bases with the other base(s), which induces

CC transcription with stress on endoplasmic reticulum used for stress

CC competence of endoplasmic reticulum. Also described are: (1) a DNA

CC having transcription inducing activity with stress on endoplasmic

CC reticulum containing the above mentioned element, optionally further

CC containing a promoter DNA; and (2) a vector containing the element

CC optionally with the DNA. The element can be used for the inhibition of

CC growth and induction of apoptosis of cancer cells, and improvement of

CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of

CC autoantibody formation. AAZ25632 to AAZ25657 represent elements used in

CC an example from the present invention.

XX SQ Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other;

Query Match 52.6%; Score 10; DB 20; Length 19;

Best Local Similarity 52.6%; Pred. No. 1.8e+03;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 1 CCAATNNNNN NNNCCACG 19

Db 1 CCAATCGGCGCTCCACG 19

|||||

RESULT 4

AAZ25634

```

ID AA225634 standard; DNA; 19 BP.
XX AC
XX AA225634;
XX DT
XX 23-DEC-1999 (first entry)
XX DE
XX Endoplasmic reticulum stress competence control element SEQ ID NO:7.
XX KW
XX Endoplasmic reticulum; ER; stress competence; control element;
XX KW inhibition; growth; apoptosis; cancer; autoimmune disease;
XX KW cystic fibrosis; ds.
XX OS
XX Rattus sp.
XX PN
XX JPI1243959-A.
XX PD
XX 14-SEP-1999.
XX PF
XX 04-MAR-1998; 98JP-0052453.
XX PR
XX 04-MAR-1998; 98JP-0052453.
XX PA
XX (HSPK-) HSP KENKYUSHO KK.
XX DR
XX WPI; 1999-603708/52.
XX PT
XX New control element for stress competence of endoplasmic reticulum -
XX useful for inhibition of growth and induction of apoptosis in cancer
XX cells
XX PS
XX Example 1; Fig 3; 25pp; Japanese.
XX CC
XX The present invention specifically claims an element shown by: (A) a
XX 19 bp base sequence, CCAATNNNNN NNNCCAG (ERSE); or (B) a modified base
XX sequence having replaced 1-3 bases with the other base(s), which induces
XX transcription with stress on endoplasmic reticulum used for stress
XX competence of endoplasmic reticulum. Also described are: (1) a DNA
XX having transcription inducing activity with stress on endoplasmic
XX reticulum containing the above mentioned element, optionally further
XX containing a promoter DNA; and (2) a vector containing the element
XX optionally with the DNA. The element can be used for the inhibition of
XX growth and induction of apoptosis of cancer cells, and improvement of
XX symptoms of autoimmune diseases and cystic fibrosis by inhibition of
XX autoantibody formation. AA225632 to AA225657 represent elements used in
XX an example from the present invention.
XX SQ
XX Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other;

Query Match 52.6%; Score 10; DB 20; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNN NNNCCAG 19
Db 1 CCAATCGGAGGCTCCAG 19

RESULT 5
AAZ25635
ID AA225635 standard; DNA; 19 BP.
XX AC
XX AAZ25635;
XX DT
XX 23-DEC-1999 (first entry)
XX DE
XX Endoplasmic reticulum stress competence control element SEQ ID NO:8.
XX KW
XX Endoplasmic reticulum; ER; stress competence; control element;
XX KW inhibition; growth; apoptosis; cancer; autoimmune disease;
XX KW cystic fibrosis; ds.
XX OS
XX Homo sapiens.
XX PT

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PN JPI1243959-A.
XX PD
XX 14-SEP-1999.
XX PF
XX 04-MAR-1998; 98JP-0052453.
XX PR
XX 04-MAR-1998; 98JP-0052453.
XX PA
XX (HSPK-) HSP KENKYUSHO KK.
XX DR
XX WPI; 1999-603708/52.
XX PT
XX New control element for stress competence of endoplasmic reticulum -
XX useful for inhibition of growth and induction of apoptosis in cancer
XX cells
XX PS
XX Example 1; Fig 3; 25pp; Japanese.
XX CC
XX The present invention specifically claims an element shown by: (A) a
XX 19 bp base sequence, CCAATNNNNN NNNCCAG (ERSE); or (B) a modified base
XX sequence having replaced 1-3 bases with the other base(s), which induces
XX transcription with stress on endoplasmic reticulum used for stress
XX competence of endoplasmic reticulum. Also described are: (1) a DNA
XX having transcription inducing activity with stress on endoplasmic
XX reticulum containing the above mentioned element, optionally further
XX containing a promoter DNA; and (2) a vector containing the element
XX optionally with the DNA. The element can be used for the inhibition of
XX growth and induction of apoptosis of cancer cells, and improvement of
XX symptoms of autoimmune diseases and cystic fibrosis by inhibition of
XX autoantibody formation. AA225632 to AA225657 represent elements used in
XX an example from the present invention.
XX SQ
XX Sequence 19 BP; 4 A; 10 C; 4 G; 1 T; 0 other;

Query Match 52.6%; Score 10; DB 20; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNN NNNCCAG 19
Db 1 CCAATCGCGCCGACCAG 19

RESULT 6
AAZ25636
ID AA225636 standard; DNA; 19 BP.
XX AC
XX AAZ25636;
XX DT
XX 23-DEC-1999 (first entry)
XX DE
XX Endoplasmic reticulum stress competence control element SEQ ID NO:9.
XX KW
XX Endoplasmic reticulum; ER; stress competence; control element;
XX KW inhibition; growth; apoptosis; cancer; autoimmune disease;
XX KW cystic fibrosis; ds.
XX OS
XX Gallus sp.
XX PN
XX JPI1243959-A.
XX PD
XX 14-SEP-1999.
XX PF
XX 04-MAR-1998; 98JP-0052453.
XX PR
XX 04-MAR-1998; 98JP-0052453.
XX PA
XX (HSPK-) HSP KENKYUSHO KK.
XX DR
XX WPI; 1999-603708/52.
XX PT
XX New control element for stress competence of endoplasmic reticulum -
XX useful for inhibition of growth and induction of apoptosis in cancer

```

```

PT cells
XX
PS Example 1; Fig 3; 25pp; Japanese.
XX
CC The present invention specifically claims an element shown by: (A) a
CC 19 bp base sequence, CCAATNNNN NNNCCACG (ERSE); or (B) a modified base
CC sequence having replaced 1-3 bases with the other base(s), which induces
CC transcription with stress on endoplasmic reticulum used for stress
CC competence of endoplasmic reticulum. Also described are: (1) a DNA
CC having transcription inducing activity with stress on endoplasmic
CC reticulum containing the above mentioned element, optionally further
CC containing a promoter DNA; and (2) a vector containing the element
CC optionally with the DNA. The element can be used for the inhibition of
CC growth and induction of apoptosis of cancer cells, and improvement of
CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
CC autoantibody formation. AAZ25632 to AAZ25657 represent elements used in
CC an example from the present invention.
XX
SQ Sequence 19 BP; 5 A; 7 C; 6 G; 1 T; 0 other;
    Query Match      52.6%; Score 10; DB 20; Length 19;
    Best Local Similarity 52.6%; Pred. No. 1.8e+03;
    Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      1 CCAATNNNNNNNNCCACG 19
      |||||
Db      1 CCAATGGGAGCGCACCACG 19
      |||||

RESULT 7
AAZ25637
ID AAZ25637 standard; DNA; 19 BP.
XX
AC AAZ25637;
XX
DT 23-DEC-1999 (first entry)
XX
DE Endoplasmic reticulum stress competence control element SEQ ID NO:10.
XX
KW Endoplasmic reticulum; ER; stress competence; control element;
KW inhibition; growth; apoptosis; cancer; autoimmune disease;
KW cystic fibrosis; ds.
XX
OS Homo sapiens.
XX
PN JP11243959-A.
XX
PD 14-SEP-1999.
XX
PF 04-MAR-1998; 98JP-0052453.
XX
PR 04-MAR-1998; 98JP-0052453.
XX
PA (HSPK-) HSP KENKYUSHO KK.
XX
DR WPI; 1999-603708/52.
XX
PT New control element for stress competence of endoplasmic reticulum -
PT useful for inhibition of growth and induction of apoptosis in cancer
PT cells
XX
PS Example 1; Fig 3; 25pp; Japanese.
XX
CC The present invention specifically claims an element shown by: (A) a
CC 19 bp base sequence, CCAATNNNN NNNCCACG (ERSE); or (B) a modified base
CC sequence having replaced 1-3 bases with the other base(s), which induces
CC transcription with stress on endoplasmic reticulum used for stress
CC competence of endoplasmic reticulum. Also described are: (1) a DNA
CC having transcription inducing activity with stress on endoplasmic
CC reticulum containing the above mentioned element, optionally further
CC containing a promoter DNA; and (2) a vector containing the element
CC optionally with the DNA. The element can be used for the inhibition of
CC growth and induction of apoptosis of cancer cells, and improvement of
CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
CC autoantibody formation. AAZ25632 to AAZ25657 represent elements used in
CC an example from the present invention.
XX
SQ Sequence 19 BP; 6 A; 6 C; 6 G; 1 T; 0 other;
    Query Match      52.6%; Score 10; DB 20; Length 19;
    Best Local Similarity 52.6%; Pred. No. 1.8e+03;
    Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      1 CCAATNNNNNNNNCCACG 19
      |||||
Db      1 CCAATCGAAGGAGCCACG 19
      |||||

RESULT 8
AAZ25638
ID AAZ25638 standard; DNA; 19 BP.
XX
AC AAZ25638;
XX
DT 23-DEC-1999 (first entry)
XX
DE Endoplasmic reticulum stress competence control element SEQ ID NO:11.
XX
KW Endoplasmic reticulum; ER; stress competence; control element;
KW inhibition; growth; apoptosis; cancer; autoimmune disease;
KW cystic fibrosis; ds.
XX
OS Gallus sp.
XX
PN JP11243959-A.
XX
PD 14-SEP-1999.
XX
PF 04-MAR-1998; 98JP-0052453.
XX
PR 04-MAR-1998; 98JP-0052453.
XX
PA (HSPK-) HSP KENKYUSHO KK.
XX
DR WPI; 1999-603708/52.
XX
PT New control element for stress competence of endoplasmic reticulum -
PT useful for inhibition of growth and induction of apoptosis in cancer
PT cells
XX
PS Example 1; Fig 3; 25pp; Japanese.
XX
CC The present invention specifically claims an element shown by: (A) a
CC 19 bp base sequence, CCAATNNNN NNNCCACG (ERSE); or (B) a modified base
CC sequence having replaced 1-3 bases with the other base(s), which induces
CC transcription with stress on endoplasmic reticulum used for stress
CC competence of endoplasmic reticulum. Also described are: (1) a DNA
CC having transcription inducing activity with stress on endoplasmic
CC reticulum containing the above mentioned element, optionally further
CC containing a promoter DNA; and (2) a vector containing the element
CC optionally with the DNA. The element can be used for the inhibition of
CC growth and induction of apoptosis of cancer cells, and improvement of
CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
CC autoantibody formation. AAZ25632 to AAZ25657 represent elements used in
CC an example from the present invention.
XX
SQ Sequence 19 BP; 4 A; 9 C; 5 G; 1 T; 0 other;
    Query Match      52.6%; Score 10; DB 20; Length 19;
    Best Local Similarity 52.6%; Pred. No. 1.8e+03;
    Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      1 CCAATNNNNNNNNCCACG 19
      |||||
Db      1 CCAATCGACGCGGCCACG 19
      |||||

```

```

RESULT 9
AAZ25639
ID AAZ25639 standard; DNA; 19 BP.
XX
AC AAZ25639;
XX
DT 23-DEC-1999 (first entry)
XX
DE Endoplasmic reticulum stress competence control element SEQ ID NO:12.
XX
KW Endoplasmic reticulum; ER; stress competence; control element;
KW inhibition; growth; apoptosis; cancer; autoimmune disease;
KW cystic fibrosis; ds.
XX
OS Homo sapiens.
XX
PN JP11243959-A.
XX
PD 14-SEP-1999.
XX
PF 04-MAR-1998; 98JP-0052453.
XX
PR 04-MAR-1998; 98JP-0052453.
XX
PA (HSPK-) HSP KENKYUSHO KK.
XX
DR WPI; 1999-603708/52.
XX
PT New control element for stress competence of endoplasmic reticulum -
PT useful for inhibition of growth and induction of apoptosis in cancer
PT cells
XX
PS Example 1; Fig 3; 25pp; Japanese.
XX
CC The present invention specifically claims an element shown by: (A) a
CC 19 bp base sequence, CCAATNNNN NNNCCACG (ERSE); or (B) a modified base
CC sequence having replaced 1-3 bases with the other base(s), which induces
CC transcripion with stress on endoplasmic reticulum used for stress
CC competence of endoplasmic reticulum. Also described are: (1) a DNA
CC having transcription inducing activity with stress on endoplasmic
CC reticulum containing the above mentioned element, optionally further
CC containing a promoter DNA; and (2) a vector containing the element
CC optionally with the DNA. The element can be used for the inhibition of
CC growth and induction of apoptosis of cancer cells, and improvement of
CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
CC autoantibody formation. AAZ25632 to AAZ25657 represent elements used in
CC an example from the present invention.
XX
SQ Sequence 19 BP; 5 A; 6 C; 5 G; 3 T; 0 other;

Query Match 52.6%; Score 10; DB 20; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
    |||||
DB 1 CCAATGATGTCGACCACG 19
    |||||

RESULT 10
AAZ25640
ID AAZ25640 standard; DNA; 19 BP.
XX
AC AAZ25640;
XX
DT 23-DEC-1999 (first entry)
XX
DE Endoplasmic reticulum stress competence control element SEQ ID NO:13.
XX
KW Endoplasmic reticulum; ER; stress competence; control element;
KW inhibition; growth; apoptosis; cancer; autoimmune disease;
KW cystic fibrosis; ds.
XX
OS Homo sapiens.
XX
PN JP11243959-A.
XX
PD 14-SEP-1999.
XX
PF 04-MAR-1998; 98JP-0052453.
XX
PR 04-MAR-1998; 98JP-0052453.
XX
PA (HSPK-) HSP KENKYUSHO KK.
XX
DR WPI; 1999-603708/52.
XX
PT New control element for stress competence of endoplasmic reticulum -
PT useful for inhibition of growth and induction of apoptosis in cancer
PT cells
XX
PS Example 1; Fig 3; 25pp; Japanese.
XX
CC The present invention specifically claims an element shown by: (A) a
CC 19 bp base sequence, CCAATNNNN NNNCCACG (ERSE); or (B) a modified base
CC sequence having replaced 1-3 bases with the other base(s), which induces
CC transcripion with stress on endoplasmic reticulum used for stress
CC competence of endoplasmic reticulum. Also described are: (1) a DNA
CC having transcription inducing activity with stress on endoplasmic
CC reticulum containing the above mentioned element, optionally further
CC containing a promoter DNA; and (2) a vector containing the element
CC optionally with the DNA. The element can be used for the inhibition of
CC growth and induction of apoptosis of cancer cells, and improvement of
CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
CC autoantibody formation. AAZ25632 to AAZ25657 represent elements used in
CC an example from the present invention.
XX
SQ Sequence 19 BP; 5 A; 6 C; 5 G; 3 T; 0 other;

Query Match 52.6%; Score 10; DB 20; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
    |||||
DB 1 CCAATGATGTCGACCACG 19
    |||||

RESULT 11
AAZ28570
ID AAA28570 standard; DNA; 19 BP.
XX
AC AAA28570;
XX
DT 29-AUG-2000 (first entry)
XX
DE GRP78 promoter ERSE1-like sequence.
XX
KW Endoplasmic reticulum; stress; ER; transcription factor;
KW transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
KW prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing;
KW cystic fibrosis; ulcer; gene therapy; recombinant gene; human;
KW gene expression; GRP; glucose regulated protein; promoter; ss.
XX
OS Homo sapiens.
XX
PN WO200029429-A2.
XX
PD 25-MAY-2000.
XX
PF 12-NOV-1999; 99WO-JP06305.
XX
PR 13-NOV-1998; 98JP-0324227.
PR 09-JUN-1999; 99JP-0163112.
XX

```

```

PA (HSPR-) HSP RES INST INC.
XX
PI Haze K, Yoshida H, Mori K, Yanagi H, Yura T;
XX
XX WPI; 2000-387736/33.
DR
XX
XX New endoplasmic reticulum stress transcription factor (known as bZIP)
XX PT for controlling expression of endoplasmic reticulum chaperone, useful
XX PT for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
XX PT diseases, wounds and ulcers
XX
PS Example 1; Fig 3; 157pp; English.
XX
XX An endoplasmic reticulum stress transcription factor (bZIP)
XX CC capable of regulating transcription inducing activity exhibited by an
XX CC element (ERSE) can be used in a method for controlling expression of
XX CC an endoplasmic reticulum chaperone. The method comprises expressing
XX CC bZIP. The method can be used for expression of a foreign protein by
XX CC positively regulating expression of an endoplasmic reticulum
XX CC chaperone gene. bZIP is useful for controlling the expression of
XX CC endoplasmic reticulum chaperone either positively or negatively in
XX CC cells and therefore is useful for treatment or prophylaxis of
XX CC cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases,
XX CC wounds and ulcers. bZIP also maintains the correct conformation of
XX CC the endoplasmic reticulum chaperone and thereby increases the
XX CC expression of a foreign protein. This sequence taken from the
XX CC glucose regulating protein (GRP) promoter GRP78 contains an ERSE like
XX CC sequence.
XX SQ Sequence 19 BP; 3 A; 9 C; 5 G; 2 T; 0 other;
XX
XX Query Match 52.6%; Score 10; DB 21; Length 19;
XX Best Local Similarity 52.6%; Pred. No. 1.8e+03;
XX Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX
Oy 1 CCAATNNNNNNNNCCACG 19
Db 1 CCAATCGCGCGCTCCACG 19
XX
XX RESULT 12
XX ID AAA28571 standard; DNA; 19 BP.
XX AC AAA28571;
XX
XX 29-AUG-2000 (first entry)
XX
XX GRP78 promoter ERSE1-like sequence.
XX
XX Endoplasmic reticulum; stress; ER; transcription factor;
XX KW transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
XX KW prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing;
XX KW cystic fibrosis; ulcer; gene therapy; recombinant gene; mouse;
XX KW gene expression; GRP; glucose regulated protein; promoter; ss.
XX
XX Mus musculus.
XX
XX WO200029429-A2.
XX
XX 25-MAY-2000.
XX
XX 12-NOV-1999; 99WO-JP06305.
XX
XX 13-NOV-1998; 98JP-0324227.
XX
XX 09-JUN-1999; 99JP-0163112.
XX
XX (HSPR-) HSP RES INST INC.
XX
XX Haze K, Yoshida H, Mori K, Yanagi H, Yura T;
XX
XX WPI; 2000-387736/33.
XX
XX New endoplasmic reticulum stress transcription factor (known as bZIP)
XX PT for controlling expression of endoplasmic reticulum chaperone, useful
XX PT for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
XX PT diseases, wounds and ulcers
XX
PS Example 1; Fig 3; 157pp; English.
XX
XX An endoplasmic reticulum stress transcription factor (bZIP)
XX CC capable of regulating transcription inducing activity exhibited by an
XX CC element (ERSE) can be used in a method for controlling expression of
XX CC an endoplasmic reticulum chaperone. The method comprises expressing
XX CC bZIP. The method can be used for expression of a foreign protein by
XX CC positively regulating expression of an endoplasmic reticulum
XX CC chaperone gene. bZIP is useful for controlling the expression of
XX CC endoplasmic reticulum chaperone either positively or negatively in
XX CC cells and therefore is useful for treatment or prophylaxis of
XX CC cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases,
XX CC wounds and ulcers. bZIP also maintains the correct conformation of
XX CC the endoplasmic reticulum chaperone and thereby increases the
XX CC expression of a foreign protein. This sequence taken from the
XX CC glucose regulating protein (GRP) promoter GRP78 contains an ERSE like
XX CC sequence.
XX SQ Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other;
XX
XX Query Match 52.6%; Score 10; DB 21; Length 19;
XX Best Local Similarity 52.6%; Pred. No. 1.8e+03;
XX Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX
Oy 1 CCAATNNNNNNNNCCACG 19
Db 1 CCAATCGCGCGCTCCACG 19
XX
XX RESULT 13
XX ID AAA28572 standard; DNA; 19 BP.
XX AC AAA28572;
XX
XX 29-AUG-2000 (first entry)
XX
XX GRP78 promoter ERSE1-like sequence.
XX
XX Endoplasmic reticulum; stress; ER; transcription factor;
XX KW transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
XX KW prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing;
XX KW cystic fibrosis; ulcer; gene therapy; recombinant gene; rat;
XX KW gene expression; GRP; glucose regulated protein; promoter; ss.
XX
XX Rattus rattus.
XX
XX WO200029429-A2.
XX
XX 25-MAY-2000.
XX
XX 12-NOV-1999; 99WO-JP06305.
XX
XX 13-NOV-1998; 98JP-0324227.
XX
XX 09-JUN-1999; 99JP-0163112.
XX
XX (HSPR-) HSP RES INST INC.
XX
XX Haze K, Yoshida H, Mori K, Yanagi H, Yura T;
XX
XX WPI; 2000-387736/33.
XX
XX New endoplasmic reticulum stress transcription factor (known as bZIP)
XX PT for controlling expression of endoplasmic reticulum chaperone, useful
XX PT for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
XX PT diseases, wounds and ulcers
XX
PS Example 1; Fig 3; 157pp; English.

```

XX An endoplasmic reticulum stress transcription factor (bZIP)  
 CC capable of regulating transcription inducing activity exhibited by an  
 CC element (ERSE) can be used in a method for controlling expression of  
 CC an endoplasmic reticulum chaperone. The method comprises expressing  
 CC bZIP. The method can be used for expression of a foreign protein by  
 CC positively regulating expression of an endoplasmic reticulum  
 CC chaperone gene. bZIP is useful for controlling the expression of  
 CC endoplasmic reticulum chaperone either positively or negatively in  
 CC cells and therefore is useful for treatment or prophylaxis of  
 CC cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases,  
 CC wounds and ulcers. bZIP also maintains the correct conformation of  
 CC the endoplasmic reticulum chaperone and thereby increases the  
 CC expression of a foreign protein. This sequence taken from the  
 CC glucose regulating protein (GRP) promoter GRP78 contains an ERSE like  
 CC sequence.  
 XX Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other;  
 SQ

Query Match 52.6%; Score 10; DB 21; Length 19;  
 Best Local Similarity 52.6%; Pred. No. 1.8e+03;  
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19  
 |||||  
 Db 1 CCAATCGGAGGCTCCACG 19

RESULT 14  
 AAA28573  
 ID AAA28573 standard; DNA; 19 BP.  
 AC AAA28573;  
 XX  
 DT 29-AUG-2000 (first entry)  
 XX  
 DE GRP94 promoter ERSE1-like sequence.  
 XX  
 KW Endoplasmic reticulum; stress; ER; transcription factor;  
 KW transcription; regulatory element; ERSE; bZIP; chaperone; treatment;  
 KW prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing;  
 KW cystic fibrosis; ulcer; gene therapy; recombinant gene; human;  
 KW gene expression; GRP; glucose regulated protein; promoter; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200029429-A2.  
 XX  
 PD 25-MAY-2000.  
 XX  
 PF 12-NOV-1999; 99WO-JP06305.  
 XX  
 PR 13-NOV-1998; 98JP-0324227.  
 PR 09-JUN-1999; 99JP-0163112.  
 XX  
 PA (HSPR-) HSP RES INST INC.  
 XX  
 PI Haze K, Yoshida H, Mori K, Yanagi H, Yura T;  
 XX  
 DR WPI; 2000-387736/33.  
 XX  
 PS New endoplasmic reticulum stress transcription factor (known as bZIP)  
 PT for controlling expression of endoplasmic reticulum chaperone, useful  
 PT for treating cancers, arteriosclerosis, cystic fibrosis, ischemic  
 PT diseases, wounds and ulcers  
 XX  
 PS Example 1; Fig 3; 157pp; English.  
 XX  
 CC An endoplasmic reticulum stress transcription factor (bZIP)  
 CC capable of regulating transcription inducing activity exhibited by an  
 CC element (ERSE) can be used in a method for controlling expression of  
 CC an endoplasmic reticulum chaperone. The method comprises expressing  
 CC bZIP. The method can be used for expression of a foreign protein by  
 CC positively regulating expression of an endoplasmic reticulum  
 CC chaperone gene. bZIP is useful for controlling the expression of  
 CC endoplasmic reticulum chaperone either positively or negatively in  
 CC cells and therefore is useful for treatment or prophylaxis of  
 CC cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases,  
 CC wounds and ulcers. bZIP also maintains the correct conformation of  
 CC the endoplasmic reticulum chaperone and thereby increases the  
 CC expression of a foreign protein. This sequence taken from the  
 CC glucose regulating protein (GRP) promoter GRP78 contains an ERSE like  
 CC sequence.

CC positively regulating expression of an endoplasmic reticulum  
 CC chaperone gene. bZIP is useful for controlling the expression of  
 CC endoplasmic reticulum chaperone either positively or negatively in  
 CC cells and therefore is useful for treatment or prophylaxis of  
 CC cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases,  
 CC wounds and ulcers. bZIP also maintains the correct conformation of  
 CC the endoplasmic reticulum chaperone and thereby increases the  
 CC expression of a foreign protein. This sequence taken from the  
 CC glucose regulating protein (GRP) promoter GRP94 contains an ERSE like  
 CC sequence.  
 SQ Sequence 19 BP; 4 A; 10 C; 4 G; 1 T; 0 other;  
 SQ

Query Match 52.6%; Score 10; DB 21; Length 19;  
 Best Local Similarity 52.6%; Pred. No. 1.8e+03;  
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19  
 |||||  
 Db 1 CCAATCGGCGCCACACG 19

RESULT 15  
 AAA28574  
 ID AAA28574 standard; DNA; 19 BP.  
 XX  
 AC AAA28574;  
 XX  
 DT 29-AUG-2000 (first entry)  
 XX  
 DE GRP94 promoter ERSE1-like sequence.  
 XX  
 KW Endoplasmic reticulum; stress; ER; transcription factor;  
 KW transcription; regulatory element; ERSE; bZIP; chaperone; treatment;  
 KW prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing;  
 KW cystic fibrosis; ulcer; gene therapy; recombinant gene; chicken;  
 KW gene expression; GRP; glucose regulated protein; promoter; ss.  
 XX  
 OS Gallus domesticus.  
 XX  
 PN WO200029429-A2.  
 XX  
 PD 25-MAY-2000.  
 XX  
 PF 12-NOV-1999; 99WO-JP06305.  
 XX  
 PR 13-NOV-1998; 98JP-0324227.  
 PR 09-JUN-1999; 99JP-0163112.  
 XX  
 PA (HSPR-) HSP RES INST INC.  
 XX  
 PI Haze K, Yoshida H, Mori K, Yanagi H, Yura T;  
 XX  
 DR WPI; 2000-387736/33.  
 XX  
 PS New endoplasmic reticulum stress transcription factor (known as bZIP)  
 PT for controlling expression of endoplasmic reticulum chaperone, useful  
 PT for treating cancers, arteriosclerosis, cystic fibrosis, ischemic  
 PT diseases, wounds and ulcers  
 XX  
 PS Example 1; Fig 3; 157pp; English.  
 XX  
 CC An endoplasmic reticulum stress transcription factor (bZIP)  
 CC capable of regulating transcription inducing activity exhibited by an  
 CC element (ERSE) can be used in a method for controlling expression of  
 CC an endoplasmic reticulum chaperone. The method comprises expressing  
 CC bZIP. The method can be used for expression of a foreign protein by  
 CC positively regulating expression of an endoplasmic reticulum  
 CC chaperone gene. bZIP is useful for controlling the expression of  
 CC endoplasmic reticulum chaperone either positively or negatively in  
 CC cells and therefore is useful for treatment or prophylaxis of  
 CC cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases,  
 CC wounds and ulcers. bZIP also maintains the correct conformation of  
 CC the endoplasmic reticulum chaperone and thereby increases the  
 CC expression of a foreign protein. This sequence taken from the  
 CC glucose regulating protein (GRP) promoter GRP94 contains an ERSE like  
 CC sequence.

CC the endoplasmic reticulum chaperone and thereby increases the  
 CC expression of a foreign protein. This sequence taken from the  
 CC glucose regulating protein (GRP) promoter GRP94 contains an ERSE like  
 CC sequence.

XX  
 SQ Sequence 19 BP; 5 A; 7 C; 6 G; 1 T; 0 other;

Query Match 52.6%; Score 10; DB 21; Length 19;  
 Best Local Similarity 52.6%; Pred. No. 1.8e+03;  
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNCCACG 19  
 |||||  
 Db 1 CCAATGGGAGCGCACCAG 19  
 |||||

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 Job time : 257 secs

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OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 06:00:59 ; Search time 74 Seconds  
(without alignments)  
113.328 Million cell updates/sec

Title: US-09-606-804-1  
Perfect score: 19  
Sequence: 1 ccaatnnnnnnnnccacg 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	10	52.6	19	4	US-09-813-937-1		Sequence 1, Appli
2	10	52.6	205	4	US-09-313-294A-1696		Sequence 1696, Ap
3	10	52.6	261	4	US-09-389-681-206		Sequence 206, App
4	10	52.6	261	4	US-09-620-405B-206		Sequence 206, App
5	10	52.6	261	4	US-09-339-338-206		Sequence 206, App
6	10	52.6	261	4	US-09-433-826B-206		Sequence 206, App
7	10	52.6	261	4	US-09-604-287A-206		Sequence 206, App
8	10	52.6	270	4	US-09-313-294A-890		Sequence 890, App
9	10	52.6	272	1	US-08-248-474-36		Sequence 36, Appl
10	10	52.6	272	3	US-08-756-849-36		Sequence 36, Appl
11	10	52.6	282	4	US-09-252-991A-987		Sequence 987, App
12	10	52.6	285	4	US-09-252-991A-60		Sequence 60, Appl
13	10	52.6	296	2	US-08-716-942-20		Sequence 20, Appl
14	10	52.6	296	4	US-09-130-337A-20		Sequence 20, Appl
15	10	52.6	300	4	US-09-313-294A-7348		Sequence 7348, Ap
16	10	52.6	360	6	5196523-1		Patent No. 5196523
17	10	52.6	387	3	US-08-804-372A-23		Sequence 23, Appl
18	10	52.6	392	4	US-09-404-879A-372		Sequence 372, App
19	10	52.6	399	6	5196523-23		Patent No. 5196523
20	10	52.6	421	6	5196523-22		Patent No. 5196523
21	10	52.6	424	1	US-08-609-657-15		Sequence 15, Appl
22	10	52.6	432	4	US-09-252-991A-9959		Sequence 9959, Ap
23	10	52.6	457	4	US-09-702-705-861		Sequence 861, App
24	10	52.6	457	4	US-09-736-457-861		Sequence 861, App
25	10	52.6	467	3	US-09-257-584-8		Sequence 8, Appli
26	10	52.6	511	4	US-09-702-705-1138		Sequence 1138, Ap
27	10	52.6	511	4	US-09-736-457-1138		Sequence 1138, Ap

c	28	10	52.6	522	4	US-09-663-600A-149	Sequence 149, App
	29	10	52.6	531	4	US-09-222-575-123	Sequence 123, App
	30	10	52.6	531	4	US-09-389-681-123	Sequence 123, App
	31	10	52.6	531	4	US-09-620-405B-123	Sequence 123, App
	32	10	52.6	531	4	US-09-339-338-123	Sequence 123, App
	33	10	52.6	531	4	US-09-433-826B-123	Sequence 123, App
	34	10	52.6	531	4	US-09-604-287A-123	Sequence 123, App
c	35	10	52.6	584	4	US-09-663-600A-55	Sequence 55, Appli
	36	10	52.6	641	4	US-09-573-906-7	Sequence 7, Appli
c	37	10	52.6	708	4	US-09-252-991A-3364	Sequence 3364, Ap
	38	10	52.6	754	3	US-09-020-956-20	Sequence 20, Appl
	39	10	52.6	754	3	US-09-030-607-20	Sequence 20, Appl
	40	10	52.6	754	4	US-09-439-313-20	Sequence 20, Appl
	41	10	52.6	754	4	US-09-352-616A-20	Sequence 20, Appl
	42	10	52.6	754	4	US-09-232-149A-20	Sequence 20, Appl
	43	10	52.6	770	4	US-09-573-906-6	Sequence 6, Appli
	44	10	52.6	843	4	US-09-171-209-38	Sequence 38, Appl
	45	10	52.6	849	3	US-08-998-416-552	Sequence 552, App

ALIGNMENTS

RESULT 1  
US-09-813-937-1  
; Sequence 1, Application US/09813937  
; Patent No. 6506600  
; GENERAL INFORMATION:  
; APPLICANT: HERMONAT, Paul L.  
; APPLICANT: MANE, Michael  
; APPLICANT: LIU, Yong  
; TITLE OF INVENTION: SECRETING PRODUCTS FROM SKIN BY ADENO-ASSOCIATED VIRUS (AAV) GEN  
; TITLE OF INVENTION: TRANSFER  
; FILE REFERENCE: 023533/0116  
; CURRENT APPLICATION NUMBER: 2001-03-22  
; PRIOR FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: US 60/191092  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 1  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: glucose response element  
; NAME/KEY: misc feature  
; LOCATION: (6)-(14)  
; OTHER INFORMATION: "N" at positions 6 - 14 can be A, C, G or T  
US-09-813-937-1

Query Match 52.6%; Score 10; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19  
Db 1 CCAATNNNNNNNNCCACG 19

RESULT 2  
US-09-313-294A-1696/c  
; Sequence 1696, Application US/09313294A  
; Patent No. 6476212  
; GENERAL INFORMATION:  
; APPLICANT: Lalugudi, Raghunath V.  
; APPLICANT: Ito, Laura F.  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
; FILE REFERENCE: PL-0017 US  
; CURRENT APPLICATION NUMBER: US/09/313,294A  
; CURRENT FILING DATE: 1999-05-14

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; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 1696
; LENGTH: 205
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700551354H1
US-09-313-294A-1696

Query Match          52.6%; Score 10; DB 4; Length 205;
Best Local Similarity 52.6%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
Db 122 CCAATCAGACAGCCACG 104

RESULT 3
US-09-389-681-206
; Sequence 206, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-389-681-206

Query Match          52.6%; Score 10; DB 4; Length 261;
Best Local Similarity 52.6%; Pred. No. 5.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
Db 140 CCAATTCCTCATCTCCACG 158

RESULT 4
US-09-620-405B-206
; Sequence 206, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-620-405B-206

Query Match          52.6%; Score 10; DB 4; Length 261;
Best Local Similarity 52.6%; Pred. No. 5.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
Db 140 CCAATTCCTCATCTCCACG 158

RESULT 5
US-09-339-338-206
; Sequence 206, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-339-338-206

Query Match          52.6%; Score 10; DB 4; Length 261;
Best Local Similarity 52.6%; Pred. No. 5.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
Db 140 CCAATTCCTCATCTCCACG 158

RESULT 6
US-09-433-826B-206
; Sequence 206, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-433-826B-206

Query Match          52.6%; Score 10; DB 4; Length 261;
Best Local Similarity 52.6%; Pred. No. 5.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
Db 140 CCAATTCCTCATCTCCACG 158
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RESULT 7
US-09-604-287A-206
; Sequence 206, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-206

Query Match 52.6%; Score 10; DB 4; Length 261;
Best Local Similarity 52.6%; Pred. No. 5.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNCCACG 19
Db 140 CCAATTCCTCATCTCCACG 158

RESULT 8
US-09-313-294A-890/c
; Sequence 890, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 890
; LENGTH: 270
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700550018H1
; NAME/KEY: unsure
; LOCATION: 213-215, 218-221, 232-233, 236-237, 239-240, 242, 249, 251, 253, 261,
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-890

Query Match 52.6%; Score 10; DB 4; Length 270;
Best Local Similarity 52.6%; Pred. No. 5.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNCCACG 19
Db 121 CCAATCAGACAGACCACG 103

RESULT 9
US-08-248-474-36
; Sequence 36, Application US/08248474
; Patent No. 5612471
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; GENERAL INFORMATION:
; APPLICANT: MCK, BIRD, David
; APPLICANT: WILSON, Mark A.
; TITLE OF INVENTION: NEMATODE-INDUCE GENES IN TOMATO
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,474
; FILING DATE: 25-MAY-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 2307E-535
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Lycopersicon esculentum cv 'Rutgers Large
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..272
; OTHER INFORMATION: /standard_name= "DB# 155"
US-08-248-474-36

Query Match 52.6%; Score 10; DB 1; Length 272;
Best Local Similarity 52.6%; Pred. No. 5.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNCCACG 19
Db 97 CCAATATTATTTTACCACG 115

RESULT 10
US-08-756-849-36
; Sequence 36, Application US/08756849
; Patent No. 6093810
; GENERAL INFORMATION:
; APPLICANT: Bird, David Mck.
; APPLICANT: Wilson, Mark A.
; TITLE OF INVENTION: Nematode-Induced Genes in Tomato
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/756,849  
; FILING DATE: 26-NOV-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/248,474  
; FILING DATE: 25-MAY-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 023070-053510US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 272 base pairs  
; TYPE: nucleic acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1..272  
; OTHER INFORMATION: /standard\_name= "DB# 155"  
US-08-756-849-36

Query Match 52.6%; Score 10; DB 3; Length 272;  
Best Local Similarity 52.6%; Pred. No. 5.4e+02;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19  
Db 97 CCAATATTATTTTACCACG 115

RESULT 11  
US-09-252-991A-987  
; Sequence 987, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 987  
; LENGTH: 282  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-987

Query Match 52.6%; Score 10; DB 4; Length 282;  
Best Local Similarity 52.6%; Pred. No. 5.4e+02;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19  
Db 49 CCAATGCTGATCCCCACG 67

RESULT 12  
US-09-252-991A-60  
; Sequence 60, Application US/09252991A

; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 60  
; LENGTH: 285  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-60

Query Match 52.6%; Score 10; DB 4; Length 285;  
Best Local Similarity 52.6%; Pred. No. 5.5e+02;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19  
Db 224 CCAATGACCGATACCACG 242

RESULT 13  
US-08-716-942-20/C  
; Sequence 20, Application US/08716942  
; Patent No. 5849491  
; GENERAL INFORMATION:  
; APPLICANT: Terragen Diversity Inc.  
; APPLICANT: Radowski, Christopher C. A.  
; APPLICANT: Seow, Kah Tong  
; APPLICANT: Warren, R. Antony J.  
; APPLICANT: Yap, Wai Ho  
; TITLE OF INVENTION: METHOD FOR ISOLATING XYLANASE GENE  
; TITLE OF INVENTION: SEQUENCES FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD AT  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Oppedahl & Larson  
; STREET: 1992 Commerce Street, Suite 309  
; CITY: Yorktown Heights  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10598-4412  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: Word Perfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/716,942  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/004,157  
; FILING DATE: 20-Sep-95  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marina T. Larson  
; REGISTRATION NUMBER: 32,038  
; REFERENCE/DOCKET NUMBER: TERR.P-001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (914) 245-3252  
; TELEFAX: (914) 962-4330  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 296  
; TYPE: nucleic acid

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; STRANDEDNESS: DOUBLE
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM:
; NAME/KEY: fragment of xylanase gene from degenerate primer
; NAME/KEY: amplification of soil DNA
US-08-716-942-20

Query Match          52.6%; Score 10; DB 2; Length 296;
Best Local Similarity 52.6%; Pred. No. 5.5e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
Db 217 CCAATGGTGTGGCCACG 199

RESULT 14
US-09-130-337A-20/c
; Sequence 20, Application US/09130337A
; Patent No. 6441148
; GENERAL INFORMATION:
; APPLICANT: Radomski, CCA
; APPLICANT: Seow, KT
; APPLICANT: Warren, RAJ
; APPLICANT: Yad, WH
; TITLE OF INVENTION: METHOD FOR AMPLIFICATION OF XYLANASE GENE FRAGMENTS
; TITLE OF INVENTION: FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD AND COMPOSITION
; TITLE OF INVENTION: THEREBY
; FILE REFERENCE: 9993-004
; CURRENT APPLICATION NUMBER: US/09/130,337A
; CURRENT FILING DATE: 1998-08-06
; PRIOR APPLICATION NUMBER: 08/716,942
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 60/004,157
; PRIOR FILING DATE: 1995-09-22
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 20
; LENGTH: 296
; TYPE: DNA
; ORGANISM: Unknown organism
; FEATURE:
; OTHER INFORMATION: Description of unknown organism: soil microbe
US-09-130-337A-20

Query Match          52.6%; Score 10; DB 4; Length 296;
Best Local Similarity 52.6%; Pred. No. 5.5e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
Db 217 CCAATGGTGTGGCCACG 199

RESULT 15
US-09-313-294A-7348/c
; Sequence 7348, Application US/0913294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program

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; SEQ ID NO 7348
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700381587H1
; NAME/KEY: unsure
; LOCATION: 18, 228, 295
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-7348

Query Match          52.6%; Score 10; DB 4; Length 300;
Best Local Similarity 52.6%; Pred. No. 5.5e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
Db 292 CCAATCGTACCTCCACG 274

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Job time : 77 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 07:13:09 ; Search time 259 Seconds  
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243.816 Million cell updates/sec

Title: US-09-606-804-1

Perfect score: 19  
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Listing first 45 summaries

Database : Published Applications NA:  
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2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	10	52.6	19	14	US-10-340-759-1
2	10	52.6	24	11	US-09-940-185-207
3	10	52.6	25	9	US-09-402-100-35
4	10	52.6	25	11	US-09-940-185-4188
5	10	52.6	100	10	US-09-969-373-1152
6	10	52.6	123	10	US-09-867-701-3962
7	10	52.6	136	12	US-09-922-449B-18
8	10	52.6	136	12	US-09-922-449B-19
9	10	52.6	142	12	US-09-922-449B-8
10	10	52.6	143	12	US-09-922-449B-24
11	10	52.6	149	12	US-09-922-449B-25
12	10	52.6	150	12	US-09-922-449B-10
13	10	52.6	167	14	US-10-001-883-5
14	10	52.6	210	10	US-09-974-300-8096
15	10	52.6	214	9	US-09-778-320-59
16	10	52.6	214	9	US-09-910-689-59

C	17	10	52.6	214	13	US-10-010-742-59	Sequence 59, Appl
	18	10	52.6	219	10	US-09-783-590-10136	Sequence 10136, A
	19	10	52.6	225	14	US-10-060-036-3284	Sequence 3284, Ap
	20	10	52.6	237	9	US-09-777-564-1013	Sequence 1013, Ap
	21	10	52.6	237	14	US-10-015-219-1013	Sequence 1013, Ap
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C	23	10	52.6	247	10	US-09-878-574-6181	Sequence 6181, Ap
	24	10	52.6	261	9	US-09-604-287A-206	Sequence 206, App
	25	10	52.6	261	10	US-09-339-338-206	Sequence 206, App
	26	10	52.6	261	11	US-09-551-621-206	Sequence 206, App
	27	10	52.6	261	12	US-10-124-805-206	Sequence 206, App
	28	10	52.6	261	13	US-10-007-805-206	Sequence 206, App
	29	10	52.6	261	14	US-10-076-622-206	Sequence 206, App
	30	10	52.6	262	12	US-10-099-926-1836	Sequence 1836, Ap
	31	10	52.6	262	13	US-10-033-528-1836	Sequence 1836, Ap
	32	10	52.6	267	9	US-09-294-093B-1896	Sequence 1896, Ap
	33	10	52.6	268	9	US-09-923-876-5857	Sequence 5857, Ap
C	34	10	52.6	271	10	US-09-783-590-11139	Sequence 11139, A
C	35	10	52.6	272	11	US-09-835-976B-57	Sequence 57, Appl
C	36	10	52.6	274	10	US-09-867-701-5278	Sequence 5278, Ap
	37	10	52.6	280	10	US-09-878-574-246	Sequence 246, App
	38	10	52.6	283	9	US-09-294-093B-3259	Sequence 3259, Ap
	39	10	52.6	293	9	US-09-294-093B-6179	Sequence 6179, Ap
C	40	10	52.6	301	11	US-09-918-995-24371	Sequence 24371, A
	41	10	52.6	306	10	US-09-974-300-8100	Sequence 8100, Ap
C	42	10	52.6	339	10	US-09-878-574-1186	Sequence 1186, Ap
	43	10	52.6	348	11	US-09-899-495-18	Sequence 18, Appl
C	44	10	52.6	351	10	US-09-938-842A-1451	Sequence 1451, Ap
	45	10	52.6	351	10	US-09-796-692-6226	Sequence 6226, Ap

## ALIGNMENTS

## RESULT 1

US-10-340-759-1  
; Sequence 1, Application US/10340759  
; Publication No. US20030104575A1  
; GENERAL INFORMATION:  
; APPLICANT: HERMONAT, Paul L.  
; APPLICANT: MANE, Michael  
; APPLICANT: LIU, Yong  
; TITLE OF INVENTION: SECRETING PRODUCTS FROM SKIN BY ADENO-ASSOCIATED VIRUS (AAV) GEN  
; FILE REFERENCE: 023533/0116  
; CURRENT APPLICATION NUMBER: US/10/340,759  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: US/09/813,937A  
; PRIOR FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: US 60/191092  
; PRIOR FILING DATE: 2000-03-22  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 1  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: glucose response element  
; NAME/KEY: misc feature  
; LOCATION: (6)-(14)  
; OTHER INFORMATION: "N" at positions 6 - 14 can be A, C, G or T  
US-10-340-759-1

Query Match 52.6%; Score 10; DB 14; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCAATNNNNNNNNCCACG 19  
Db 1 CCAATNNNNNNNNNNCCACG 19

```

RESULT 2
US-09-940-185-207/c
; Sequence 207, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 207
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-207

Query Match          52.6%; Score 10; DB 11; Length 24;
Best Local Similarity 52.6%; Pred. No. 4.2e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
    |||||
Db 23 CCAATATTACGTGACCACG 5

RESULT 3
US-09-402-100-35/c
; Sequence 35, Application US/09402100
; Patent No. US20010019834A1
; GENERAL INFORMATION:
; APPLICANT: Daewoong Pharmaceutical Co, LTD
; APPLICANT: Kim, Byung-O
; APPLICANT: Shin, Sung-Seup
; APPLICANT: Yu, Young-Hyo
; APPLICANT: Park, Myung-Hwan
; APPLICANT: Choi, Deok-Joon
; APPLICANT: Jung, Hyung-Jin
; TITLE OF INVENTION: Recombinant Microorganisms Expressing Antigenic Proteins of Helio
; FILE REFERENCE: 0136/OG140
; CURRENT APPLICATION NUMBER: US/09/402,100
; CURRENT FILING DATE: 1999-09-27
; EARLIER APPLICATION NUMBER: KR 97-11950
; EARLIER FILING DATE: 1997-03-31
; EARLIER APPLICATION NUMBER: KR 97-11951
; EARLIER FILING DATE: 1997-03-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ( )..(?)
; OTHER INFORMATION: Oligonucleotide
US-09-402-100-35

Query Match          52.6%; Score 10; DB 9; Length 25;
Best Local Similarity 52.6%; Pred. No. 4.2e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
    |||||
Db 23 CCAATATTACGTGACCACG 5

RESULT 4
US-09-940-185-4188/c
; Sequence 4188, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4188
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-4188

Query Match          52.6%; Score 10; DB 11; Length 25;
Best Local Similarity 52.6%; Pred. No. 4.2e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
    |||||
Db 24 CCAATATTACGTGACCACG 6

RESULT 5
US-09-969-373-1152/c
; Sequence 1152, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 1152
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-1152

Query Match          52.6%; Score 10; DB 10; Length 100;
Best Local Similarity 52.6%; Pred. No. 4.9e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
    |||||
Db 97 CCAATCATTTCCATCCACG 79

RESULT 6
US-09-867-701-3962
; Sequence 3962, Application US/09867701
```

Db 20 CCAATTTTACCATCCACG 2

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; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3962
; LENGTH: 123
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-3962

Query Match      52.6%; Score 10; DB 10; Length 123;
Best Local Similarity 52.6%; Pred. No. 5e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy      1 CCAATNNNNNNNNCCACG 19
      |||||
Db      4 CCAATCTGTCGGACCACG 22

RESULT 7
US-09-922-449B-18
; Sequence 18, Application US/09922449B
; Publication No. US20030148278A1
; GENERAL INFORMATION:
; APPLICANT: BioInside Gesellschaft fur Biodiagnostik, Auftragsforschung und Consulting
; APPLICANT: mbH
; TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically mod
; TITLE OF INVENTION: in foodstuff by means of fluorescent-coupled PCR
; FILE REFERENCE: 101215-68
; CURRENT APPLICATION NUMBER: US/09/922,449B
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: PCT/EP00/009835
; PRIOR FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: DE 199 06 169.6
; PRIOR FILING DATE: 1999-02-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 136
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: target IAC DNA for the Bt-176
US-09-922-449B-18

Query Match      52.6%; Score 10; DB 12; Length 136;
Best Local Similarity 52.6%; Pred. No. 5.1e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy      1 CCAATNNNNNNNNCCACG 19
      |||||
Db      27 CCAATTTTCGCTCCACG 45

RESULT 8
US-09-922-449B-19
; Sequence 19, Application US/09922449B
; Publication No. US20030148278A1
; GENERAL INFORMATION:
; APPLICANT: BioInside Gesellschaft fur Biodiagnostik, Auftragsforschung und Consulting
; APPLICANT: mbH
; TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically mod
; TITLE OF INVENTION: in foodstuff by means of fluorescent-coupled PCR
; FILE REFERENCE: 101215-68
```

```
; CURRENT APPLICATION NUMBER: US/09/922,449B
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: PCT/EP00/009835
; PRIOR FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: DE 199 06 169.6
; PRIOR FILING DATE: 1999-02-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 136
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: reference IAC DNA for the B
; OTHER INFORMATION: 176 maize gen
US-09-922-449B-19

Query Match      52.6%; Score 10; DB 12; Length 136;
Best Local Similarity 52.6%; Pred. No. 5.1e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy      1 CCAATNNNNNNNNCCACG 19
      |||||
Db      27 CCAATTTTCGCTCCACG 45

RESULT 9
US-09-922-449B-8
; Sequence 8, Application US/09922449B
; Publication No. US20030148278A1
; GENERAL INFORMATION:
; APPLICANT: BioInside Gesellschaft fur Biodiagnostik, Auftragsforschung und Consulting
; APPLICANT: mbH
; TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically mod
; TITLE OF INVENTION: in foodstuff by means of fluorescent-coupled PCR
; FILE REFERENCE: 101215-68
; CURRENT APPLICATION NUMBER: US/09/922,449B
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: PCT/EP00/009835
; PRIOR FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: DE 199 06 169.6
; PRIOR FILING DATE: 1999-02-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 142
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: target IAC DNA for the RRS 9
US-09-922-449B-8

Query Match      52.6%; Score 10; DB 12; Length 142;
Best Local Similarity 52.6%; Pred. No. 5.1e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy      1 CCAATNNNNNNNNCCACG 19
      |||||
Db      31 CCAATTTTCGCTCCACG 49

RESULT 10
US-09-922-449B-24
; Sequence 24, Application US/09922449B
; Publication No. US20030148278A1
; GENERAL INFORMATION:
; APPLICANT: BioInside Gesellschaft fur Biodiagnostik, Auftragsforschung und Consulting
; APPLICANT: mbH
; TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically mod
; TITLE OF INVENTION: in foodstuff by means of fluorescent-coupled PCR
; FILE REFERENCE: 101215-68
; CURRENT APPLICATION NUMBER: US/09/922,449B
; CURRENT FILING DATE: 2001-08-03
```

; PRIOR APPLICATION NUMBER: PCT/EP00/009835  
; PRIOR FILING DATE: 2000-02-07  
; PRIOR APPLICATION NUMBER: DE 199 06 169.6  
; PRIOR FILING DATE: 1999-02-08  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 24  
; LENGTH: 143  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: target IAC DNA for the RRS ge  
US-09-922-449B-24

Query Match 52.6%; Score 10; DB 12; Length 143;  
Best Local Similarity 52.6%; Pred. No. 5.1e+03;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19  
|||||  
Db 31 CCAATTTTCGCCTCCACG 49

## RESULT 11

US-09-922-449B-25  
; Sequence 25, Application US/09922449B  
; Publication No. US20030148278A1  
; GENERAL INFORMATION:  
; APPLICANT: Bioinside Gesellschaft fur Bodiagnostik, Auftragsforschung und Consulting  
; APPLICANT: mbH  
; TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically modified  
; TITLE OF INVENTION: in foodstuff by means of fluorescent-coupled PCR  
; FILE REFERENCE: 101215-68  
; CURRENT APPLICATION NUMBER: US/09/922,449B  
; PRIOR APPLICATION NUMBER: 2001-08-03  
; PRIOR FILING DATE: 2000-02-07  
; PRIOR APPLICATION NUMBER: DE 199 06 169.6  
; PRIOR FILING DATE: 1999-02-08  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 25  
; LENGTH: 149  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: reference IAC DNA for the RRS  
US-09-922-449B-25

Query Match 52.6%; Score 10; DB 12; Length 149;  
Best Local Similarity 52.6%; Pred. No. 5.1e+03;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19  
|||||  
Db 31 CCAATTTTCGCCTCCACG 49

## RESULT 12

US-09-922-449B-10  
; Sequence 10, Application US/09922449B  
; Publication No. US20030148278A1  
; GENERAL INFORMATION:  
; APPLICANT: Bioinside Gesellschaft fur Bodiagnostik, Auftragsforschung und Consulting  
; APPLICANT: mbH  
; TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically modified  
; TITLE OF INVENTION: in foodstuff by means of fluorescent-coupled PCR  
; FILE REFERENCE: 101215-68  
; CURRENT APPLICATION NUMBER: US/09/922,449B  
; PRIOR APPLICATION NUMBER: 2001-08-03  
; PRIOR FILING DATE: 2000-02-07  
; PRIOR APPLICATION NUMBER: PCT/EP00/009835  
; PRIOR FILING DATE: 2000-02-07

; PRIOR APPLICATION NUMBER: DE 199 06 169.6  
; PRIOR FILING DATE: 1999-02-08  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 150  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: reference IAC DNA for the RRS  
; OTHER INFORMATION: gen  
US-09-922-449B-10

Query Match 52.6%; Score 10; DB 12; Length 150;  
Best Local Similarity 52.6%; Pred. No. 5.1e+03;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19  
|||||  
Db 32 CCAATTTTCGCCTCCACG 50

## RESULT 13

US-10-001-883-5/c  
; Sequence 5, Application US/10001883  
; Publication No. US20030022188A1  
; GENERAL INFORMATION:  
; APPLICANT: Macina, Roberto  
; APPLICANT: Recipon, Hervé  
; APPLICANT: Pluta, Jason  
; APPLICANT: Ghosh, Malavika  
; APPLICANT: Sun, Yongming  
; APPLICANT: Liu, Chenghua  
; TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Pri  
; FILE REFERENCE: DEX-0271  
; CURRENT APPLICATION NUMBER: US/10/001,883  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/252,059  
; PRIOR FILING DATE: 2000-11-20  
; NUMBER OF SEQ ID NOS: 137  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 167  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-001-883-5

Query Match 52.6%; Score 10; DB 14; Length 167;  
Best Local Similarity 52.6%; Pred. No. 5.2e+03;  
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19  
|||||  
Db 160 CCAATTTTGAATCACCACG 142

## RESULT 14

US-09-974-300-8096/c  
; Sequence 8096, Application US/09974300  
; Patent No. US20020146721A1  
; GENERAL INFORMATION:  
; APPLICANT: Berka, Randy M.  
; APPLICANT: Clausen, Ib Groth  
; TITLE OF INVENTION: Methods for Monitoring Multiple Gene  
; TITLE OF INVENTION: Expression  
; FILE REFERENCE: 10085,500-US  
; CURRENT APPLICATION NUMBER: US/09/974,300  
; CURRENT FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: 09/680,598  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/279,526  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 8481

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8096
; LENGTH: 210
; TYPE: DNA
; ORGANISM: Bacillus clausii
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(210)
; OTHER INFORMATION: n = A,T,C or G
US-09-974-300-8096

Query Match      52.6%; Score 10; DB 10; Length 210;
Best Local Similarity 52.6%; Pred. No. 5.3e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy      1 CCAATNNNNNNCCACG 19
      |||||
Db      152 CCAATTCTGCTGTCACG 134

RESULT 15
US-09-778-320-59/c
; Sequence 59, Application US/09778320
; Patent No. US20010034052A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, TongTong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491CS
; CURRENT APPLICATION NUMBER: US/09/778,320
; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 214
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(214)
; OTHER INFORMATION: n = A,T,C or G
US-09-778-320-59

Query Match      52.6%; Score 10; DB 9; Length 214;
Best Local Similarity 52.6%; Pred. No. 5.3e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy      1 CCAATNNNNNNCCACG 19
      |||||
Db      88 CCAATTCTTCATCTCCACG 70

Search completed: December 4, 2003, 08:51:36
Job time : 263 secs

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